

# SEQUENCE LISTING

<110> O'Donnell, Michael E.  
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Kuriyan, John

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT  
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND  
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 60/143,202

<151> 1997-04-08

<150> 08/823,407

<151> 1997-04-08

<150> 09/057,416

<151> 1998-04-08

<160> 212

<170> PatentIn Ver. 2.1

<210> 1

<211> 2007

<212> DNA

<213> *Thermus thermophilus*

<400> 1

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2007

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<210> 2

<211> 529

<212> PRT

<213> *Thermus thermophilus*

<400> 2

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Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
      20              25              30

```

```

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
      35              40              45

```

```

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
      50              55              60

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Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
      65              70              75              80

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Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
      85              90              95

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Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro			
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Gly	Arg	Ala	Leu	Ala	Ala	Glu	Ala	Leu	Pro	Gln	Pro	Thr	Gly	Ala	Pro			
			340					345					350					

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro  
 355 360 365  
 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe  
 370 375 380  
 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg  
 385 390 395 400  
 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys  
 405 410 415  
 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro  
 420 425 430  
 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu  
 435 440 445  
 Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro  
 450 455 460  
 Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Glu Val Glu Ala Glu  
 465 470 475 480  
 Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg  
 485 490 495  
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 <212> DNA  
 <213> Thermus thermophilus

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 ttctccgggc ccaggggcgt gggcaagacc accacggcga ggctcctcgc catggcggtg 180  
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<210> 4

<211> 464

<212> PRT

<213> *Thermus thermophilus*

<400> 4

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```

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
      20              25              30

```

```

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
    35              40              45

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Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
    50              55              60

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```

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
    65              70              75              80

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```

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
      85              90              95

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Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu  
 100 105 110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser  
 115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro  
 130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro  
 145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu  
 165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg  
 180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly  
 195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu  
 210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro  
 225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr  
 245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala  
 260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu  
 275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln  
 290 295 300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu  
 305 310 315 320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala  
 325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro  
 340 345 350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro  
 355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe  
 370 375 380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg  
 385 390 395 400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys  
 405 410 415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro  
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Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu  
 435 440 445

Gly Glu Lys Lys Lys Pro Glu Pro Lys Ala Pro Pro Gly Pro Thr Ser  
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<210> 5

<211> 454

<212> PRT

<213> Thermus thermophilus

<400> 5

Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val  
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Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu  
 20 25 30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly  
 35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly  
 50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg  
 65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser

	85		90		95
Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu	100		105		110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser	115		120		125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro	130		135		140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro	145		150		155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu	165		170		175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg	180		185		190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly	195		200		205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu	210		215		220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro	225		230		235
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr	245		250		255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala	260		265		270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu	275		280		285
Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln	290		295		300
Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu	305		310		315
Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala	325		330		335
Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro					



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Ser	Pro	Glu	Val	Gly	Pro	Lys	Pro	Glu	Ser	Pro	Pro	Thr	Pro	Glu	Pro
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Pro	Glu	Val	Arg	Glu	Gly	Gln	Leu	Cys	Leu	Ala	Phe	Pro	Glu	Asp	Lys
			405				410						415		
Ala	Phe	His	Tyr	Arg	Lys	Ala	Ser	Glu	Gln	Lys	Val	Arg	Leu	Leu	Pro
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Leu	Ala	Gln	Ala	His	Phe	Gly	Val	Glu	Glu	Val	Val	Leu	Val	Leu	Glu
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Gly	Glu	Lys	Lys	Lys	Ala										
	450														

<210> 6  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 6  
 cgcaagcttc acgcstacct sttctccggs ac 32

<210> 7  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: peptide

<400> 7  
 His Ala Tyr Leu Phe Ser Gly Thr  
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<210> 8  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 8  
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34

<210> 9  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 9  
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1 5

<210> 10  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

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38

<210> 11  
<211> 38  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 11  
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38

<210> 12  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

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<210> 13  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 13  
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27

<210> 14  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 14  
gcgcgaattc gggcgcttca ggaggtggg

29

<210> 15  
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<212> DNA  
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<223> Description of Artificial Sequence: primer

<400> 15  
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31

<210> 16  
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<212> DNA  
<213> Artificial Sequence

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<400> 16  
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31

<210> 17  
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<212> PRT  
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<220>  
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<223> X is any aa at position 2

<220>  
<221> PEPTIDE  
<222> (3)  
<223> X is any aa at position 3

<220>  
<221> PEPTIDE  
<222> (5)  
<223> X is any aa at position 5

<400> 17  
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<210> 18  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 18

Lys Pro Asp Pro Lys Ala Pro Pro Gly Pro Thr Ser  
1 5 10

<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala  
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu  
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly  
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys  
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg  
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala  
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln  
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val  
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu  
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln  
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys  
165 170 175

Ala Leu Asp Val  
180

<210> 20  
 <211> 180  
 <212> PRT  
 <213> Bacillus subtilis

<400> 20  
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 Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly  
 35 40 45  
 Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys  
 50 55 60  
 Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys  
 65 70 75 80  
 Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala  
 85 90 95  
 Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys  
 100 105 110  
 Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val  
 115 120 125  
 His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu  
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 Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His  
 145 150 155 160  
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 Arg Ile Thr Ser  
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<210> 21  
 <211> 294  
 <212> PRT

<213> Escherichia coli

<400> 21

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Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
  1              5              10              15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
      20              25              30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
      35              40              45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
      50              55              60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
      65              70              75              80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
      85              90              95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
      100             105             110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
      115             120             125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
      130             135             140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
      145             150             155             160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
      165             170             175

Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn
      180             185             190

Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg
      195             200             205

Ala Ala Glu Gly Ser Leu Arg Asp Ala Leu Ser Leu Thr Asp Gln Ala
      210             215             220

Ile Ala Ser Gly Asp Gly Gln Val Ser Thr Gln Ala Val Ser Ala Met
      225             230             235             240
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Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met  
245 250 255

Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala  
260 265 270

Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu  
275 280 285

Leu His Arg Ile Ala Met  
290

<210> 22  
<211> 294  
<212> PRT  
<213> Haemophilus influenzae

<400> 22

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala  
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu  
20 25 30

Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly  
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys  
50 55 60

Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys  
65 70 75 80

Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala  
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln  
100 105 110

Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val  
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu  
130 135 140

Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln  
145 150 155 160



Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys  
165 170 175

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr  
180 185 190

Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys  
195 200 205

Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala  
210 215 220

Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met  
225 230 235 240

Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu  
245 250 255

His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala  
260 265 270

Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys  
275 280 285

Leu His Gln Ile Ala Leu  
290

<210> 23

<211> 294

<212> PRT

<213> Bacillus subtilis

<400> 23

Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu  
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu  
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly  
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys  
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys

65		70		75		80
Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala						
	85		90		95	
Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys						
	100		105		110	
Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val						
	115		120		125	
His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu						
	130		135		140	
Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His						
	145		150		155	160
Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys						
	165		170		175	
Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp						
	180		185		190	
Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser						
	195		200		205	
Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala						
	210		215		220	
Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile						
	225		230		235	240
Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu						
	245		250		255	
His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu						
	260		265		270	
Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr						
	275		280		285	
Phe Arg Asp Met Leu Leu						
	290					

<210> 24  
 <211> 300  
 <212> PRT

<213> Caulobacter crescentus

<400> 24

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Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu
  1              5              10              15

Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
      20              25              30

Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
      35              40              45

Val Gly Lys Thr Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
      50              55              60

Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
      65              70              75              80

Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
      85              90              95

Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
      100             105             110

Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile
      115             120             125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
      130             135             140

Lys Thr Leu Glu Glu Pro Pro Pro His Ala Lys Phe Ile Phe Ala Thr
      145             150             155             160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
      165             170             175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
      180             185             190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
      195             200             205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
      210             215             220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
      225             230             235             240
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Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile  
245 250 255

Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu  
260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met  
275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val  
290 295 300

<210> 25

<211> 260

<212> PRT

<213> Mycoplasma genitalium

<400> 25

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln  
1 5 10 15

Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn  
20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr  
35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu  
50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser  
65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser  
85 90 95

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn  
100 105 110

His Pro Phe Thr Phe Lys Lys Lys Val Tyr Ile Leu Asp Glu Ala His  
115 120 125

Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu  
130 135 140

Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Thr Glu Phe Asn Lys  
145 150 155 160

Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys  
165 170 175

Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys  
180 185 190

Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu  
195 200 205

Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala  
210 215 220

Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His  
225 230 235 240

Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Lys Gln Phe  
245 250 255

Tyr Gln Glu Ile  
260

<210> 26

<211> 289

<212> PRT

<213> Thermus thermophilus

<400> 26

Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val  
1 5 10 15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu  
20 25 30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly  
35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly  
50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg  
65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser  
85 90 95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu

100	105	110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
115	120	125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
165	170	175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
180	185	190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly		
195	200	205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
210	215	220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	235
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
245	250	255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
260	265	270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
275	280	285

Tyr

<210> 27

<211> 94

<212> DNA

<213> Thermus thermophilus

<400> 27

gccggaggga	gaaaaaaaaa	gccgagccca	aggccccgcc	cgccccacc	ccgaagcgcc	60
cgcacccccg	ggccccccga	ggaggaggag	aggc			94

<210> 28  
<211> 11  
<212> PRT  
<213> Thermus thermophilus

<400> 28  
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro  
1 5 10

<210> 29  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<220>  
<221> unsure  
<222> (6)  
<223> N at position 6 is either G or C

<220>  
<221> unsure  
<222> (12)  
<223> N at position 12 is either G or C

<220>  
<221> unsure  
<222> (21)  
<223> N at position 21 is either G or C

<400> 29  
cacgcntacc tnttctccgg nac

23

<210> 30  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<220>  
<221> unsure

<222> (7)  
<223> N at position 7 is either G or C

<220>  
<221> unsure  
<222> (10)  
<223> N at position 10 is either G or C

<220>  
<221> unsure  
<222> (19)  
<223> N at position 19 is either G or C

<220>  
<221> unsure  
<222> (22)  
<223> N at position 22 is either G or C

<400> 30  
gtgctcnggn ggctcctcnt cngtc 25

<210> 31  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 31  
gtgggatccg tggttctgga tctcgatgaa gaa 33

<210> 32  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 32  
gtgggatcca cggststcs gagcagaag 29

<210> 33  
<211> 34



<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33

gcgggatacct caacgaggac ctctccatct tcaa

34

<210> 34

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 34

gcgggatacct tgtcgtsag sgtsagsgcg tcgta

35

<210> 35

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 35

gggaaggacc agcgcgtact cccctgctc ctaggtgtg

39

<210> 36

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 36

gtgtggatcc ttcttcttsc ccatsgc

27

<210> 37

<211> 27

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 37  
 caccgattcc agtggtgcct aggtgtg 27  
  
  
 <210> 38  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 38  
 caacacctgg tgttcagga gcctgtgctt 30  
  
  
 <210> 39  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 39  
 ccagaatcgt ctgctggtcg tag 23  
  
  
 <210> 40  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 40  
 agcaccctgg aggagcttc 19  
  
  
 <210> 41  
 <211> 19

<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 41  
catgtcgtac tgggtgtac

19

<210> 42  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (7)

<223> N at position 7 is A, C, G, or T

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (13)

<223> N at position 13 is A, C, G, or T

<220>

<221> unsure

<222> (14)

<223> N at position 14 is A, C, G, or T

<400> 42  
gtsgtsnnsg acnnsgagac sacsggg

27

<210> 43  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (9)

<223> N at position 9 is A, C, G, or T

<220>

<221> unsure

<222> (17)

<223> N at position 17 is A, C, G, or T

<220>

<221> unsure

<222> (18)

<223> N at position 18 is A, C, G, or T

<400> 43

gaasccsnng tcgaasnngg cgttgtg

27

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

cggggatcca cctcaatcac ctcggtg

27

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45

cggggatccg ccaccttgcg gctccgggtg

30

<210> 46  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 46  
gcgctctaga cgagttccca aagcgtgcgg t 31

<210> 47  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 47  
cgcgctctaga tcacctgtat ccaga 25

<210> 48  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 48  
gcggcgcata tgggtggtggt cctggacctg gag 33

<210> 49  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 49  
cgcgctctaga tcacctgtat ccaga 25

<210> 50  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 50  
 gtsctsgttsa agacscactt 20  
  
 <210> 51  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 51  
 sagsagsgcg ttgaasgtgt g 21  
  
 <210> 52  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 52  
 ctcggttggtg aaagtttccg tg 22  
  
 <210> 53  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 53  
 ctcggttggtg aaagtttccg tg 22

<210> 54  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 54  
 tctggcaaca cgttctggag cacatcc 27  
  
 <210> 55  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 55  
 tgctggcggt catcttcagg atg 23  
  
 <210> 56  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 56  
 catcctgaag atgaacgcca gca 23  
  
 <210> 57  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 57  
 aggttatcca caggggtcat gtgca 25

<210> 58  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 58  
gtgtgtcata tgaacataac gggtcccaa 29

<210> 59  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 59  
gcgcgaattc tcccttgtgg aaggcttag 29

<210> 60  
<211> 13  
<212> PRT  
<213> Thermus thermophilus

<400> 60  
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp  
1 5 10

<210> 61  
<211> 14  
<212> PRT  
<213> Thermus thermophilus

<400> 61  
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys  
1 5 10

<210> 62  
<211> 8



<212> PRT  
<213> Thermus thermophilus

<400> 62  
Phe Phe Ile Glu Ile Gln Asn His  
1 5

<210> 63  
<211> 8  
<212> PRT  
<213> Thermus thermophilus

<400> 63  
Tyr Asp Ala Leu Thr Leu Asp Asp  
1 5

<210> 64  
<211> 6  
<212> PRT  
<213> Thermus thermophilus

<400> 64  
Ala Met Gly Lys Lys Lys  
1 5

<210> 65  
<211> 9  
<212> PRT  
<213> Thermus thermophilus

<400> 65  
Phe Asn Lys Ser His Ser Ala Ala Tyr  
1 5

<210> 66  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<221> PEPTIDE

<222> (3)  
<223> Xaa at position 3 is undefined

<220>  
<221> PEPTIDE  
<222> (5)  
<223> Xaa at position 5 is undefined

<400> 66  
Val Val Xaa Asp Xaa Glu Thr Thr Gly  
1 5

<210> 67  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<221> PEPTIDE  
<222> (4)  
<223> Xaa at position 4 is undefined

<220>  
<221> PEPTIDE  
<222> (7)  
<223> Xaa at position 7 is undefined

<400> 67  
His Asn Ala Xaa Phe Asp Xaa Gly Phe  
1 5

<210> 68  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<221> PEPTIDE  
<222> (3)  
<223> Xaa at position 3 is undefined

<220>  
<221> PEPTIDE  
<222> (5)  
<223> Xaa at position 5 is undefined

<400> 68  
Val Val Xaa Asp Xaa Glu Thr Thr Gly  
1 5

<210> 69  
<211> 7  
<212> PRT  
<213> Thermus thermophilus

<400> 69  
Val Leu Val Lys Thr His Leu  
1 5

<210> 70  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 70  
His Arg Ala Leu Tyr Asp  
1 5

<210> 71  
<211> 7  
<212> PRT  
<213> Thermus thermophilus

<400> 71  
His Thr Phe Asn Ala Leu Leu  
1 5

<210> 72  
<211> 34  
<212> PRT  
<213> Escherichia coli

<400> 72

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu  
1 5 10 15

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro  
20 25 30

Val Val

<210> 73

<211> 34

<212> PRT

<213> *Vibrio cholerae*

<400> 73

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu  
1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro  
20 25 30

Val Val

<210> 74

<211> 34

<212> PRT

<213> *Haemophilus influenzae*

<400> 74

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu  
1 5 10 15

Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro  
20 25 30

Leu Val

<210> 75

<211> 34

<212> PRT

<213> *Rickettsia prowazekii*

<400> 75  
 Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln  
 1 5 10 15  
 Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro  
 20 25 30  
 Ile Val

<210> 76  
 <211> 34  
 <212> PRT  
 <213> Helicobacter pylori

<400> 76  
 Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg  
 1 5 10 15  
 Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys  
 20 25 30  
 Ile Ile

<210> 77  
 <211> 34  
 <212> PRT  
 <213> Synechocystis sp.

<400> 77  
 Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg  
 1 5 10 15  
 Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys  
 20 25 30  
 Ile Val

<210> 78  
 <211> 34  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<400> 78  
 Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg  
 1 5 10 15  
 Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro  
 20 25 30  
 Pro Leu

<210> 79  
 <211> 46  
 <212> PRT  
 <213> Escherichia coli

<400> 79  
 Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala  
 1 5 10 15  
 Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu  
 20 25 30  
 Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp  
 35 40 45

<210> 80  
 <211> 46  
 <212> PRT  
 <213> Vibrio cholerae

<400> 80  
 Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala  
 1 5 10 15  
 Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys  
 20 25 30  
 Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu  
 35 40 45

<210> 81  
 <211> 46  
 <212> PRT  
 <213> Haemophilus influenzae

<400> 81  
 Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala  
           1                  5                  10                  15  
 Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu  
                   20                  25                  30  
 Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp  
           35                  40                  45

<210> 82  
 <211> 46  
 <212> PRT  
 <213> Rickettsia prowazekii

<400> 82  
 Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp  
           1                  5                  10                  15  
 Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys  
                   20                  25                  30  
 Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp  
           35                  40                  45

<210> 83  
 <211> 45  
 <212> PRT  
 <213> Helicobacter pylori

<400> 83  
 Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser  
           1                  5                  10                  15  
 Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp  
                   20                  25                  30  
 Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln  
           35                  40                  45

<210> 84  
 <211> 46  
 <212> PRT  
 <213> Synechocystis sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys  
1 5 10 15

Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp  
20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln  
35 40 45

<210> 85

<211> 46

<212> PRT

<213> Mycobacterium tuberculosis

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser  
1 5 10 15

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp  
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp  
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

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gccttgggcca tgaccgacca cggcaacctc ttcggggccg tggagttcta caagaaggcc 180  
accgaaatgg gcatcaagcc catcctgggc tacgaggcct acgtggcggc ggaaagccgc 240  
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gccctctcgg ggtgcctcgg ggcggagatc ccccagttca tcctccagga ccgtctggac 480  
ctggccgagg cccggctcaa cgagtacctc tccatcttca aggaccgctt cttcatcgag 540  
atccagaacc acggcctccc cgagcagaaa aagggtcaacg aggtcctcaa ggagttcgcc 600  
cgaaagtacg gcctggggat ggtggccacc aacgacggcc attacgtgag gaaggaggac 660  
gcccgcgccc acgaggtcct cctcgccatc cagtccaaga gcaccctgga cgaccccggg 720  
cgctggcgct tcccctgcga cgagttctac gtgaagaccc ccgaggagat gcgggccatg 780  
ttccccgagg aggagtgggg ggacgagccc tttgacaaca ccgtggagat cgcccgcatg 840



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cccttttgg

3729

<210> 87

<211> 1245

<212> PRT

<213> *Thermus thermophilus*

<400> 87

Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe  
1 5 10 15

Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val  
20 25 30

Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly  
35 40 45

Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly  
50 55 60

Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg  
65 70 75 80

Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu  
85 90 95

Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu  
100 105 110

Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp  
115 120 125

Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly  
130 135 140

Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp  
145 150 155 160

Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg  
165 170 175

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val  
180 185 190

Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val  
195 200 205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His  
 210 215 220  
 Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly  
 225 230 235 240  
 Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu  
 245 250 255  
 Met Arg Ala Met Phe Pro Glu Glu Glu Val Gly Gly Arg Ser Pro Leu  
 260 265 270  
 Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly  
 275 280 285  
 Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg  
 290 295 300  
 Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg  
 305 310 315 320  
 Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg  
 325 330 335  
 Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu  
 340 345 350  
 Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser  
 355 360 365  
 Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe  
 370 375 380  
 His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro  
 385 390 395 400  
 Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys  
 405 410 415  
 Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val  
 420 425 430  
 Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu  
 435 440 445  
 Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile  
 450 455 460

Asp Thr Asp Phe Ser Asp Arg Glu Arg Asp Arg Val Ile Gln Tyr Val																			
465					470				475										480
Arg Glu Arg Tyr Gly Glu Asp Lys Val Ala Gln Ile Gly Thr Leu Gly																			
				485				490											495
Ser Leu Ala Ser Lys Ala Ala Leu Lys Glu Val Ala Arg Val Tyr Gly																			
			500					505								510			
Ile Pro Arg Lys Lys Ala Glu Glu Leu Ala Lys Leu Ile Pro Val Gln																			
			515				520						525						
Phe Gly Lys Pro Lys Pro Leu Gln Glu Ala Ile Gln Val Val Pro Glu																			
			530				535						540						
Leu Arg Ala Glu Met Glu Lys Asp Pro Lys Val Arg Glu Val Leu Glu																			
545					550				555										560
Val Ala Met Arg Leu Glu Gly Leu Asn Arg His Ala Ser Val His Ala																			
				565				570											575
Gly Arg Gly Gly Val Phe Ser Glu Pro Leu Thr Asp Leu Val Pro Leu																			
			580					585								590			
Cys Ala Thr Arg Lys Gly Gly Pro Tyr Thr Gln Tyr Asp Met Gly Ala																			
			595					600								605			
Val Glu Ala Leu Gly Leu Leu Lys Met Asp Phe Leu Gly Leu Arg Thr																			
			610				615						620						
Leu Thr Phe Leu Asp Glu Val Lys Arg Ile Val Lys Ala Ser Gln Gly																			
625					630				635										640
Val Glu Leu Asp Tyr Asp Ala Leu Pro Leu Asp Asp Pro Lys Thr Phe																			
				645					650										655
Ala Leu Leu Ser Arg Gly Glu Thr Lys Gly Val Phe Gln Leu Glu Ser																			
			660					665											670
Gly Gly Met Thr Ala Thr Leu Arg Gly Leu Lys Pro Arg Arg Phe Glu																			
			675					680								685			
Asp Leu Ile Ala Ile Leu Ser Leu Tyr Arg Pro Gly Pro Met Glu His																			
			690				695						700						
Ile Pro Thr Tyr Ile Arg Arg His His Gly Leu Glu Pro Val Ser Tyr																			
705					710							715							720

Ser Glu Phe Pro His Ala Glu Lys Tyr Leu Lys Pro Ile Leu Asp Glu  
                     725                    730                    735

Thr Tyr Gly Ile Pro Val Tyr Gln Glu Gln Ile Met Gln Ile Ala Ser  
                     740                    745                    750

Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser  
                     755                    760                    765

Met Gly Lys Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe  
                     770                    775                    780

Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Glu Ala Asn Arg  
 785                    790                    795                    800

Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser  
                     805                    810                    815

His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys  
                     820                    825                    830

Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg  
                     835                    840                    845

His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met  
                     850                    855                    860

Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe  
 865                    870                    875                    880

Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn  
                     885                    890                    895

Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly  
                     900                    905                    910

Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys  
                     915                    920                    925

Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu  
                     930                    935                    940

Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu  
 945                    950                    955                    960

Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met  
                     965                    970                    975

Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro  
 980 985 990  
 Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile  
 995 1000 1005  
 Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr  
 1010 1015 1020  
 Ala Thr Cys Thr Leu Glu Glu Leu Pro His Leu Ala Arg Asp Leu Pro  
 1025 1030 1035 1040  
 Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg  
 1045 1050 1055  
 Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp  
 1060 1065 1070  
 Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln  
 1075 1080 1085  
 Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu  
 1090 1095 1100  
 Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp  
 1105 1110 1115 1120  
 Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val  
 1125 1130 1135  
 Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu  
 1140 1145 1150  
 Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly  
 1155 1160 1165  
 Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu  
 1170 1175 1180  
 Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu  
 1185 1190 1195 1200  
 Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg  
 1205 1210 1215  
 Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala  
 1220 1225 1230

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu  
1235 1240 1245

<210> 88

<211> 198

<212> PRT

<213> *Thermus thermophilus*

<400> 88

Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu  
1 5 10 15

Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly  
20 25 30

Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu  
35 40 45

Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg  
50 55 60

Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg  
65 70 75 80

Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro  
85 90 95

Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala  
100 105 110

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro  
115 120 125

Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser  
130 135 140

Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu  
145 150 155 160

Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg  
165 170 175

Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr  
180 185 190

Tyr Met Leu Thr Ser Gly  
195

<210> 89  
 <211> 182  
 <212> PRT  
 <213> Deinococcus radiodurans

<220>  
 <221> PEPTIDE  
 <222> (79)  
 <223> X at position 79 is undefined

<400> 89  
 Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe  
 1 5 10 15  
 Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val  
 20 25 30  
 Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro  
 35 40 45  
 Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg  
 50 55 60  
 Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys  
 65 70 75 80  
 Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val  
 85 90 95  
 Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu  
 100 105 110  
 Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln  
 115 120 125  
 Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val  
 130 135 140  
 Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg  
 145 150 155 160  
 Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu  
 165 170 175  
 Glu Leu Leu Gly Glu Arg  
 180



<210> 90  
 <211> 201  
 <212> PRT  
 <213> Bacillus subtilis

<400> 90

His	Gly	Ile	Lys	Met	Ile	Tyr	Gly	Met	Glu	Ala	Asn	Leu	Val	Asp	Asp
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Gly	Val	Pro	Ile	Ala	Tyr	Asn	Ala	Ala	His	Arg	Leu	Leu	Glu	Glu	Glu
			20					25					30		
Thr	Tyr	Val	Val	Phe	Asp	Val	Glu	Thr	Thr	Gly	Leu	Ser	Ala	Val	Tyr
		35						40				45			
Asp	Thr	Ile	Ile	Glu	Leu	Ala	Ala	Val	Lys	Val	Lys	Gly	Gly	Glu	Ile
	50					55					60				
Ile	Asp	Lys	Phe	Glu	Ala	Phe	Ala	Asn	Pro	His	Arg	Pro	Leu	Ser	Ala
65					70					75				80	
Thr	Ile	Ile	Glu	Leu	Thr	Gly	Ile	Thr	Asp	Asp	Met	Leu	Gln	Asp	Ala
			85						90					95	
Pro	Asp	Val	Val	Asp	Val	Ile	Arg	Asp	Phe	Arg	Glu	Trp	Ile	Gly	Asp
		100						105					110		
Asp	Ile	Leu	Val	Ala	His	Asn	Ala	Ser	Phe	Asp	Met	Gly	Phe	Leu	Asn
		115					120					125			
Val	Ala	Tyr	Lys	Lys	Leu	Leu	Glu	Val	Glu	Lys	Ala	Lys	Asn	Pro	Val
	130					135					140				
Ile	Asp	Thr	Leu	Glu	Leu	Gly	Arg	Phe	Leu	Tyr	Pro	Glu	Phe	Lys	Asn
145				150					155					160	
His	Arg	Leu	Asn	Thr	Leu	Cys	Lys	Lys	Phe	Asp	Ile	Glu	Leu	Thr	Gln
			165						170					175	
His	His	Arg	Ala	Ile	Tyr	Asp	Thr	Glu	Ala	Thr	Ala	Tyr	Leu	Leu	Leu
		180					185						190		
Lys	Met	Leu	Lys	Asp	Ala	Ala	Glu	Lys							
	195						200								

<210> 91  
 <211> 188  
 <212> PRT  
 <213> Haemophilus influenzae

<220>  
 <221> PEPTIDE  
 <222> (47)  
 <223> X at position 47 is undefined

<220>  
 <221> PEPTIDE  
 <222> (57)  
 <223> X at position 57 is undefined

<400> 91  
 Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly  
     1                    5                    10                    15  
 Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile  
                     20                    25                    30  
 Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His  
                     35                    40                    45  
 Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val  
                     50                    55                    60  
 His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu  
                     65                    70                    75                    80  
 Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile  
                     85                    90                    95  
 His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys  
                     100                    105                    110  
 Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr  
                     115                    120                    125  
 Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp  
                     130                    135                    140  
 Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His  
                     145                    150                    155                    160  
 Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met  
                     165                    170                    175

Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu  
180 185

<210> 92

<211> 189

<212> PRT

<213> Escherichia coli

<400> 92

Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr  
1 5 10 15

Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu  
20 25 30

Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe  
35 40 45

His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val  
50 55 60

His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu  
65 70 75 80

Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile  
85 90 95

His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp Tyr Glu Phe Ser Leu  
100 105 110

Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp  
115 120 125

Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu  
130 135 140

Asp Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg Thr Leu  
145 150 155 160

His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala  
165 170 175

Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu  
180 185

<210> 93  
 <211> 201  
 <212> PRT  
 <213> Helicobacter pylori

<400> 93  
 Asn Leu Glu Tyr Leu Lys Ala Cys Gly Leu Asn Phe Ile Glu Thr Ser  
   1                  5                  10                  15  
 Glu Asn Leu Ile Thr Leu Lys Asn Leu Lys Thr Pro Leu Lys Asp Glu  
                   20                  25                  30  
 Val Phe Ser Phe Ile Asp Leu Glu Thr Thr Gly Ser Cys Pro Ile Lys  
           35                  40                  45  
 His Glu Ile Leu Glu Ile Gly Ala Val Gln Val Lys Gly Gly Glu Ile  
   50                  55                  60  
 Ile Asn Arg Phe Glu Thr Leu Val Lys Val Lys Ser Val Pro Asp Tyr  
  65                  70                  75                  80  
 Ile Ala Glu Leu Thr Gly Ile Thr Tyr Glu Asp Thr Leu Asn Ala Pro  
                   85                  90                  95  
 Ser Ala His Glu Ala Leu Gln Glu Leu Arg Leu Phe Leu Gly Asn Ser  
           100                  105                  110  
 Val Phe Val Ala His Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg  
  115                  120                  125  
 Tyr Phe Val Glu Lys Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys  
  130                  135                  140  
 Thr Leu Asp Leu Ser Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu  
 145                  150                  155                  160  
 Ser Phe Leu Lys Glu Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg  
           165                  170                  175  
 Ala Tyr Ala Asp Ala Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu  
           180                  185                  190  
 Leu Asn Leu Pro Ser Tyr Ile Lys Thr  
  195                  200

<210> 94  
 <211> 630

<212> DNA

<213> *Thermus thermophilus*

<400> 94

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atggtggagc ggggtggtgcg gacccttctg gacgggaggt tcctcctgga ggagggggtg 60
gggctttggg agtggcgcta cccctttccc ctggaggggg aggcggtggt ggtcctggac 120
ctggagacca cggggcttgc cggcctggac gaggtgattg aggtgggcct cctccgcctg 180
gaggggggga ggcgcctccc cttccagagc ctcgctccggc ccctcccgcc cgccgaagcc 240
cgttcgtgga acctcaccgg catcccccg gaggccctgg aggaggcccc ctccctggag 300
gaggttctgg agaaggccta ccccctccgc ggcgaagcca ccttggtgat ccacaacgcc 360
gcctttgacc tgggcttccct ccgcccggcc ttggaggggc tgggctaccg cctggaaaac 420
cccgtggtgg actccctgcg cttggccaga cggggcttac caggccttag gcgctacggc 480
ctggacgcc tctccgaggt cctggagctt ccccgaaagga cctgccaccg ggccctcgag 540
gacgtggagc gcaccctcgc cgtggtgcac gaggtatact atatgcttac gtccggccgt 600
ccccgcacgc tttgggaact cgggaggtag                                     630
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<210> 95

<211> 210

<212> PRT

<213> *Thermus thermophilus*

<400> 95

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Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
  1                   5                   10                   15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
    20                   25                   30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
    35                   40                   45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
    50                   55                   60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
    65                   70                   75                   80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
    85                   90                   95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
    100                  105                  110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
    115                  120                  125

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
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130                      135                      140  
 Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly  
 145                      150                      155                      160  
 Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His  
                     165                      170                      175  
 Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val  
                     180                      185                      190  
 Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly  
                     195                      200                      205  
 Arg Glx  
                     210

<210> 96  
 <211> 461  
 <212> PRT  
 <213> Pseudomonas marcesans

<400> 96  
 Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn  
   1                    5                    10                    15  
 Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser  
                     20                    25                    30  
 Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser  
                     35                    40                    45  
 Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala  
                     50                    55                    60  
 Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala  
   65                    70                    75                    80  
 Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro  
                     85                    90                    95  
 Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu  
                     100                    105                    110  
 Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe  
                     115                    120                    125

Asn	Arg	Phe	Val	Val	Gly	Pro	Asn	Ser	Arg	Met	Ala	His	Ala	Ala	Ala			
130						135					140							
Met	Ala	Val	Ala	Glu	Ser	Pro	Gly	Arg	Glu	Phe	Asn	Pro	Leu	Phe	Ile			
145					150					155					160			
Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile	Gly			
				165					170					175				
His	Tyr	Arg	Leu	Glu	Ile	Asp	Pro	Gly	Ala	Lys	Val	Ser	Tyr	Val	Ser			
			180					185					190					
Thr	Glu	Thr	Phe	Thr	Asn	Asp	Leu	Ile	Leu	Ala	Ile	Arg	Gln	Asp	Arg			
		195					200					205						
Met	Gln	Ala	Phe	Arg	Asp	Arg	Tyr	Arg	Ala	Ala	Asp	Leu	Ile	Leu	Val			
	210					215					220							
Asp	Asp	Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	Phe			
225					230					235					240			
Phe	His	Thr	Phe	Asn	Ala	Leu	His	Asp	Ala	Gly	Ser	Gln	Ile	Val	Leu			
				245					250					255				
Ala	Ser	Asp	Arg	Pro	Pro	Ser	Gln	Ile	Pro	Arg	Leu	Gln	Glu	Arg	Leu			
			260					265					270					
Met	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Val	Gln	Ala	Pro	Asp			
		275					280					285						
Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	His	Glu	Arg			
	290					295					300							
Val	Gly	Leu	Pro	Arg	Asp	Leu	Ile	Gln	Phe	Ile	Ala	Gly	Arg	Phe	Thr			
305					310					315					320			
Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Thr	Arg	Ala	Ile	Ala	Phe			
				325					330					335				
Ala	Ser	Ile	Thr	Gly	Leu	Pro	Met	Thr	Val	Asp	Ser	Ile	Ala	Pro	Met			
			340					345					350					
Leu	Asp	Pro	Asn	Gly	Gln	Gly	Val	Glu	Val	Thr	Pro	Lys	Gln	Val	Leu			
	355						360					365						
Asp	Lys	Val	Ala	Glu	Val	Phe	Lys	Val	Thr	Pro	Asp	Glu	Met	Arg	Ser			
	370					375					380							

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr  
 385 390 395 400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr  
 405 410 415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val  
 420 425 430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys  
 435 440 445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg  
 450 455 460

<210> 97

<211> 447

<212> PRT

<213> Synechocystis sp.

<400> 97

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala  
 1 5 10 15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val  
 20 25 30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly  
 35 40 45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu  
 50 55 60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr  
 65 70 75 80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro  
 85 90 95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr  
 100 105 110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala  
 115 120 125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe  
 130 135 140



Leu Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile  
 145 150 155 160

Ala His Tyr Arg Leu Glu Met Tyr Pro Asn Ala Lys Val Tyr Tyr Val  
 165 170 175

Ser Thr Glu Arg Phe Thr Asn Asp Leu Ile Thr Ala Ile Arg Gln Asp  
 180 185 190

Asn Met Glu Asp Phe Arg Ser Tyr Tyr Arg Ser Ala Asp Phe Leu Leu  
 195 200 205

Ile Asp Asp Ile Gln Phe Ile Lys Gly Lys Glu Tyr Thr Gln Glu Glu  
 210 215 220

Phe Phe His Thr Phe Asn Ser Leu His Glu Ala Gly Lys Gln Val Val  
 225 230 235 240

Val Ala Ser Asp Arg Ala Pro Gln Arg Ile Pro Gly Leu Gln Asp Arg  
 245 250 255

Leu Ile Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Ile Gln Val Pro  
 260 265 270

Asp Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu Tyr Asp  
 275 280 285

Arg Ile Arg Leu Pro Lys Glu Val Ile Glu Tyr Ile Ala Ser His Tyr  
 290 295 300

Thr Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Ala Ile Ala  
 305 310 315 320

Tyr Thr Ser Leu Ser Asn Val Ala Met Thr Val Glu Asn Ile Ala Pro  
 325 330 335

Val Leu Asn Pro Pro Val Glu Lys Val Ala Ala Ala Pro Glu Thr Ile  
 340 345 350

Ile Thr Ile Val Ala Gln His Tyr Gln Leu Lys Val Glu Glu Leu Leu  
 355 360 365

Ser Asn Ser Arg Arg Arg Glu Val Ser Leu Ala Arg Gln Val Gly Met  
 370 375 380

Tyr Leu Met Arg Gln His Thr Asp Leu Ser Leu Pro Arg Ile Gly Glu  
 385 390 395 400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys  
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr  
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser  
435 440 445

<210> 98

<211> 446

<212> PRT

<213> Bacillus subtilis

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu  
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys  
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu  
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp  
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile  
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys  
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn  
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe  
115 120 125

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr  
130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu  
145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys



420                                      425                                      430  
 Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys  
       435                                      440                                      445  
  
 <210> 99  
 <211> 507  
 <212> PRT  
 <213> Mycobacterium tuberculosis  
  
 <400> 99  
 Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val  
       1                                      5                                      10                                      15  
  
 Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser  
           20                                      25                                      30  
  
 Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu  
           35                                      40                                      45  
  
 Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser  
           50                                      55                                      60  
  
 Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala  
       65                                      70                                      75                                      80  
  
 Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu  
           85                                      90                                      95  
  
 Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr  
           100                                      105                                      110  
  
 Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr  
           115                                      120                                      125  
  
 Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln  
           130                                      135                                      140  
  
 His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser  
       145                                      150                                      155                                      160  
  
 Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr  
           165                                      170                                      175  
  
 Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Ala Leu Ala  
           180                                      185                                      190

Ile Ala Glu Ala Pro Ala Arg Ala Tyr Asn Pro Leu Phe Ile Trp Gly  
 195 200 205

Glu Ser Gly Leu Gly Lys Thr His Leu Leu His Ala Ala Gly Asn Tyr  
 210 215 220

Ala Gln Arg Leu Phe Pro Gly Met Arg Val Lys Tyr Val Ser Thr Glu  
 225 230 235 240

Glu Phe Thr Asn Asp Phe Ile Asn Ser Leu Arg Asp Asp Arg Lys Val  
 245 250 255

Ala Phe Lys Arg Ser Tyr Arg Asp Val Asp Val Leu Leu Val Asp Asp  
 260 265 270

Ile Gln Phe Ile Glu Gly Lys Glu Gly Ile Gln Glu Glu Phe Phe His  
 275 280 285

Thr Phe Asn Thr Leu His Asn Ala Asn Lys Gln Ile Val Ile Ser Ser  
 290 295 300

Asp Arg Pro Pro Lys Gln Leu Ala Thr Leu Glu Asp Arg Leu Arg Thr  
 305 310 315 320

Arg Phe Glu Trp Gly Leu Ile Thr Asp Val Gln Pro Pro Glu Leu Glu  
 325 330 335

Thr Arg Ile Ala Ile Leu Arg Lys Lys Ala Gln Met Glu Arg Leu Ala  
 340 345 350

Val Pro Asp Asp Val Leu Glu Leu Ile Ala Ser Ser Ile Glu Arg Asn  
 355 360 365

Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Val Thr Ala Phe Ala Ser  
 370 375 380

Leu Asn Lys Thr Pro Ile Asp Lys Ala Leu Ala Glu Ile Val Leu Arg  
 385 390 395 400

Asp Leu Ile Ala Asp Ala Asn Thr Met Gln Ile Ser Ala Ala Thr Ile  
 405 410 415

Met Ala Ala Thr Ala Glu Tyr Phe Asp Thr Thr Val Glu Glu Leu Arg  
 420 425 430

Gly Pro Gly Lys Thr Arg Ala Leu Ala Gln Ser Arg Gln Ile Ala Met  
 435 440 445

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln  
 450 455 460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile  
 465 470 475 480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu  
 485 490 495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg  
 500 505

<210> 100  
 <211> 446  
 <212> PRT  
 <213> Thermus thermophilus

<400> 100  
 Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg  
 1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro  
 20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe  
 35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly  
 50 55 60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val  
 65 70 75 80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro  
 85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly  
 100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser  
 115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu  
 130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg  
 145 150 155 160

Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn  
165 170 175  
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg  
180 185 190  
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe  
195 200 205  
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn  
210 215 220  
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro  
225 230 235 240  
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu  
245 250 255  
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile  
260 265 270  
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp  
275 280 285  
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp  
290 295 300  
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val  
305 310 315 320  
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro  
325 330 335  
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly  
340 345 350  
Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys  
355 360 365  
Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu  
370 375 380  
Leu Thr Pro Ala Ser Leu Pro Glu Ile Gly Gln Leu Phe Gly Gly Arg  
385 390 395 400  
Asp His Thr Thr Val Arg Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala  
405 410 415

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu  
420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly  
435 440 445

<210> 101

<211> 467

<212> PRT

<213> Escherichia coli

<400> 101

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu  
1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu  
20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu  
35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr  
50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr  
65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala  
85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser  
100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr  
115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly  
130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Ala Arg Gln Val Ala Asp Asn  
145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu  
165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg



180		185		190
Lys Pro Asn Ala Lys Val Val Tyr Met His Ser Glu Arg Phe Val Gln				
195		200		205
Asp Met Val Lys Ala Leu Gln Asn Asn Ala Ile Glu Glu Phe Lys Arg				
210		215		220
Tyr Tyr Arg Ser Val Asp Ala Leu Leu Ile Asp Asp Ile Gln Phe Phe				
225		230		235
				240
Ala Asn Lys Glu Arg Ser Gln Glu Glu Phe Phe His Thr Phe Asn Ala				
		245		250
				255
Leu Leu Glu Gly Asn Gln Gln Ile Ile Leu Thr Ser Asp Arg Tyr Pro				
		260		265
				270
Lys Glu Ile Asn Gly Val Glu Asp Arg Leu Lys Ser Arg Phe Gly Trp				
		275		280
				285
Gly Leu Thr Val Ala Ile Glu Pro Pro Glu Leu Glu Thr Arg Val Ala				
		290		295
				300
Ile Leu Met Lys Lys Ala Asp Glu Asn Asp Ile Arg Leu Pro Gly Glu				
305		310		315
				320
Val Ala Phe Phe Ile Ala Lys Arg Leu Arg Ser Asn Val Arg Glu Leu				
		325		330
				335
Glu Gly Ala Leu Asn Arg Val Ile Ala Asn Ala Asn Phe Thr Gly Arg				
		340		345
				350
Ala Ile Thr Ile Asp Phe Val Arg Glu Ala Leu Arg Asp Leu Leu Ala				
		355		360
				365
Leu Gln Glu Lys Leu Val Thr Ile Asp Asn Ile Gln Lys Thr Val Ala				
		370		375
				380
Glu Tyr Tyr Lys Ile Lys Val Ala Asp Leu Leu Ser Lys Arg Arg Ser				
385		390		395
				400
Arg Ser Val Ala Arg Pro Arg Gln Met Ala Met Ala Leu Ala Lys Glu				
		405		410
				415
Leu Thr Asn His Ser Leu Pro Glu Ile Gly Asp Ala Phe Gly Gly Arg				
		420		425
				430
Asp His Thr Thr Val Leu His Ala Cys Arg Lys Ile Glu Gln Leu Arg				

435                      440                      445  
 Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr  
 450                      455                      460  
  
 Leu Ser Ser  
 465  
  
 <210> 102  
 <211> 440  
 <212> PRT  
 <213> *Thermatoga maritima*  
  
 <400> 102  
 Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys  
 1                      5                      10                      15  
  
 Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly  
 20                      25                      30  
  
 Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu  
 35                      40                      45  
  
 Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu  
 50                      55                      60  
  
 Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His  
 65                      70                      75                      80  
  
 Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr  
 85                      90                      95  
  
 Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly  
 100                      105                      110  
  
 Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly  
 115                      120                      125  
  
 Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr  
 130                      135                      140  
  
 His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp  
 145                      150                      155                      160  
  
 Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val  
 165                      170                      175

Asp	Ser	Met	Lys	Glu	Gly	Lys	Leu	Asn	Glu	Phe	Arg	Glu	Lys	Tyr	Arg	180	185	190	
Lys	Lys	Val	Asp	Ile	Leu	Leu	Ile	Asp	Asp	Val	Gln	Phe	Leu	Ile	Gly	195	200	205	
Lys	Thr	Gly	Val	Gln	Thr	Glu	Leu	Phe	His	Thr	Phe	Asn	Glu	Leu	His	210	215	220	
Asp	Ser	Gly	Lys	Gln	Ile	Val	Ile	Cys	Ser	Asp	Arg	Glu	Pro	Gln	Lys	225	230	235	240
Leu	Ser	Glu	Phe	Gln	Asp	Arg	Leu	Val	Ser	Arg	Phe	Gln	Met	Gly	Leu	245	250	255	
Val	Ala	Lys	Leu	Glu	Pro	Pro	Asp	Glu	Glu	Thr	Arg	Lys	Ser	Ile	Ala	260	265	270	
Arg	Lys	Met	Leu	Glu	Ile	Glu	His	Gly	Glu	Leu	Pro	Glu	Glu	Val	Leu	275	280	285	
Asn	Phe	Val	Ala	Glu	Asn	Val	Asp	Asp	Asn	Leu	Arg	Arg	Leu	Arg	Gly	290	295	300	
Ala	Ile	Ile	Lys	Leu	Leu	Val	Tyr	Lys	Glu	Thr	Thr	Gly	Lys	Glu	Val	305	310	315	320
Asp	Leu	Lys	Glu	Ala	Ile	Leu	Leu	Leu	Lys	Asp	Phe	Ile	Lys	Pro	Asn	325	330	335	
Arg	Val	Lys	Ala	Met	Asp	Pro	Ile	Asp	Glu	Leu	Ile	Glu	Ile	Val	Ala	340	345	350	
Lys	Val	Thr	Gly	Val	Pro	Arg	Glu	Glu	Ile	Leu	Ser	Asn	Ser	Arg	Asn	355	360	365	
Val	Lys	Ala	Leu	Thr	Ala	Arg	Arg	Ile	Gly	Met	Tyr	Val	Ala	Lys	Asn	370	375	380	
Tyr	Leu	Lys	Ser	Ser	Leu	Arg	Thr	Ile	Ala	Glu	Lys	Phe	Asn	Arg	Ser	385	390	395	400
His	Pro	Val	Val	Val	Asp	Ser	Val	Lys	Lys	Val	Lys	Asp	Ser	Leu	Leu	405	410	415	
Lys	Gly	Asn	Lys	Gln	Leu	Lys	Ala	Leu	Ile	Asp	Glu	Val	Ile	Gly	Glu	420	425	430	

Ile Ser Arg Arg Ala Leu Ser Gly  
435 440

<210> 103

<211> 457

<212> PRT

<213> Helicobacter pylori

<400> 103

Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys  
1 5 10 15

Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln  
20 25 30

Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr  
35 40 45

Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala  
50 55 60

Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala  
65 70 75 80

His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn  
85 90 95

Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp  
100 105 110

Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val  
115 120 125

Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn  
130 135 140

Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu  
145 150 155 160

Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu  
165 170 175

Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn  
180 185 190

Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe  
195 200 205

Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu  
 210 215 220  
 Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile  
 225 230 235 240  
 Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp  
 245 250 255  
 Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro  
 260 265 270  
 Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu  
 275 280 285  
 Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His  
 290 295 300  
 Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser  
 305 310 315 320  
 Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys  
 325 330 335  
 Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu  
 340 345 350  
 Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser  
 355 360 365  
 Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys  
 370 375 380  
 Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser  
 385 390 395 400  
 Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met  
 405 410 415  
 Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Glu Lys Ser Pro Phe Val  
 420 425 430  
 Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp  
 435 440 445  
 Lys Lys Thr Ala Phe Asn Ser Ser Glu  
 450 455

<210> 104  
 <211> 1305  
 <212> DNA  
 <213> *Thermus thermophilus*

<400> 104  
 gtgtcgcacg aggccgtctg gcaacacggt ctggagcaca tccgccgcag catcaccgag 60  
 gtggagttcc acacctggtt tgaaaggatc cgccccttgg ggatccggga cggggtgctg 120  
 gagctcgccg tgcccacctc ctttgccctg gactggatcc ggcgccacta cgccggcctc 180  
 atccaggagg gccctcgggt cctcggggcc caggcgcccc ggtttgagct ccgggtggtg 240  
 cccggggtcg tagtccagga ggacatcttc cagccccgcg cgagcccccc ggcccaagct 300  
 caaccggaag atacctttaa aacttcgtgg tggggcccaa caactccatg gccccacggc 360  
 ggcgccgtgg ccgtggccga gtcccccggc cgggcctaca acccctctt catctacggg 420  
 ggccgtggcc tgggaaagac ctacctgatg cagccgtggg gccactccg tgcgaagcgc 480  
 ttccccaca tgagattaga gtacgtttcc acgaaaactt tcaccaacga gctcatcaac 540  
 cggccatccg cgagggaccg gatgacggag ttccgggagc ggtaccgctc cgtggacctc 600  
 ctgctggtgg acgacgtcca gttcatcgcc ggaaaggagc gcaccagga ggagtttttc 660  
 cacaccttca acgcccctta cgaggccac aagcagatca tcctctctc cgaccggccg 720  
 cccaaggaca tcctcaccct ggaggcgcgc ctgcgagacc gctttgagtg gggcctgac 780  
 accgacaatc cagccccga cctggaaacc cggatcgcca tcctgaagat gaacgccagc 840  
 agcgggcctg aggatcccga ggacgcctg gactacatcg cccggcaggt cacctccaac 900  
 atccgggagt gggaaggggc cctcatgagg gcatcgctt tcgcctccct caacggcggt 960  
 gagctgaccc gcgccgtggc ggccaaggct ctccgacatc ttcgccccag ggagctggag 1020  
 gcggacccct tggagatcat ccgcaaagcg gcgggaccag ttcggcctga aaccgccgga 1080  
 ggagctcacg gggagcgccg caagaaggag gtggtcctcc cccggcagct cgccatgtac 1140  
 ctggtgcggg agctcaccct ggcctccctg cccgagatcg accagctcaa cgacgaccgg 1200  
 gaccacacca cggtcctcta cgccatccag aaggtccagg agctcgcgga aagcgaccgg 1260  
 gaggtgcagg gcctcctccg caccctccgg gaggcgtgca catga 1305

<210> 105  
 <211> 434  
 <212> PRT  
 <213> *Thermus thermophilus*

<400> 105  
 Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg  
 1 5 10 15  
 Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro  
 20 25 30  
 Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe  
 35 40 45  
 Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly

50		55		60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val				
65		70		80
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro				
	85		90	95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly				
	100		105	110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser				
	115		120	125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu				
	130		135	140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg				
145		150		160
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn				
	165		170	175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg				
	180		185	190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe				
	195		200	205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn				
	210		215	220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro				
225		230		240
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu				
	245		250	255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile				
	260		265	270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp				
	275		280	285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp				
	290		295	300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val				

305		310		315		320
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro						
	325		330		335	
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly						
	340		345		350	
Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys						
	355		360		365	
Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu						
	370		375		380	
Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg						
385		390		395		400
Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala						
	405		410		415	
Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala						
	420		425		430	

Cys Thr

<210> 106  
 <211> 1128  
 <212> DNA  
 <213> *Thermus thermophilus*

<400> 106  
 atgaacataa cgggttcccaa aaaactcctc tcggaccagc tttccctcct ggagcgcatac 60  
 gtccccctcta gaagcgccaa cccctctac acctacctgg ggctttacgc cgaggaagg 120  
 gccttgatcc tcttcgggac caacggggag gtggacctcg aggtccgcct ccccgccgag 180  
 gcccaaagcc ttcccgggt gctcgtcccc gccagccct tcttcagct ggtgcggagc 240  
 cttcctgggg acctcgtggc cctcggcctc gcctcggagc cgggccaggg ggggcagctg 300  
 gagctctcct ccgggcggtt ccgcacccgg ctcagcctgg cccctgccga gggctacccc 360  
 gagcttctgg tgcccagggg ggaggacaag ggggccttcc ccctccggac gcgcatgccc 420  
 tccggggagc tcgtcaaggc cttgaccac gtgcgctacg ccgcgagcaa cgaggagtac 480  
 cgggccatct tccgcggggt gcagctggag ttctcccccc agggcttccg ggcggtggcc 540  
 tccgacgggt accgcctcgc cctctacgac ctgcccctgc cccaagggtt ccaggccaag 600  
 gccgtggtcc ccgcccggag cgtggacgag atggtgcggg tcctgaaggg ggcggacggg 660  
 gccgaggccg tcctcgcctt gggcgagggg gtgttgccc tggccctcga gggcggaagc 720  
 ggggtccgga tggccctccg cctcatggaa ggggagttcc ccgactacca gaggtcatc 780  
 cccaggagt tcgccctcaa ggtccagggt gagggggagg ccctcaggga ggcggtgcgc 840  
 cgggtgagcg tcctctccga ccggcagaac caccgggtgg acctcctttt ggaggaaggc 900



cggatcctcc tctccgccga gggggactac ggcaaggggc aggaggaggt gcccgccag 960  
 gtggaggggc cggacatggc cgtggcctac aacgcccgct acctcctcga ggccctcgcc 1020  
 cccgtggggg accgggcccc cctgggcata tccgggcccc cgagcccgag cctcatctgg 1080  
 ggggacgggg aggggtaccg ggcggtggtg gtgcccctca ggggtctag 1128

<210> 107

<211> 376

<212> PRT

<213> *Thermus thermophilus*

<400> 107

Met	Asn	Ile	Thr	Val	Pro	Lys	Lys	Leu	Leu	Ser	Asp	Gln	Leu	Ser	Leu
1				5				10					15		
Leu	Glu	Arg	Ile	Val	Pro	Ser	Arg	Ser	Ala	Asn	Pro	Leu	Tyr	Thr	Tyr
			20					25					30		
Leu	Gly	Leu	Tyr	Ala	Glu	Glu	Gly	Ala	Leu	Ile	Leu	Phe	Gly	Thr	Asn
		35					40					45			
Gly	Glu	Val	Asp	Leu	Glu	Val	Arg	Leu	Pro	Ala	Glu	Ala	Gln	Ser	Leu
	50					55					60				
Pro	Arg	Val	Leu	Val	Pro	Ala	Gln	Pro	Phe	Phe	Gln	Leu	Val	Arg	Ser
65					70					75				80	
Leu	Pro	Gly	Asp	Leu	Val	Ala	Leu	Gly	Leu	Ala	Ser	Glu	Pro	Gly	Gln
			85					90						95	
Gly	Gly	Gln	Leu	Glu	Leu	Ser	Ser	Gly	Arg	Phe	Arg	Thr	Arg	Leu	Ser
		100						105					110		
Leu	Ala	Pro	Ala	Glu	Gly	Tyr	Pro	Glu	Leu	Leu	Val	Pro	Glu	Gly	Glu
	115						120					125			
Asp	Lys	Gly	Ala	Phe	Pro	Leu	Arg	Thr	Arg	Met	Pro	Ser	Gly	Glu	Leu
	130					135					140				
Val	Lys	Ala	Leu	Thr	His	Val	Arg	Tyr	Ala	Ala	Ser	Asn	Glu	Glu	Tyr
145					150					155				160	
Arg	Ala	Ile	Phe	Arg	Gly	Val	Gln	Leu	Glu	Phe	Ser	Pro	Gln	Gly	Phe
			165					170						175	
Arg	Ala	Val	Ala	Ser	Asp	Gly	Tyr	Arg	Leu	Ala	Leu	Tyr	Asp	Leu	Pro
		180						185					190		

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val  
 195 200 205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val  
 210 215 220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser  
 225 230 235 240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr  
 245 250 255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly  
 260 265 270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg  
 275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu  
 290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln  
 305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu  
 325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly  
 340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala  
 355 360 365

Val Val Val Pro Leu Arg Val Glx  
 370 375

<210> 108

<211> 376

<212> PRT

<213> Thermus thermophilus

<400> 108

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu  
 1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr  
 20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn  
 35 40 45  
 Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu  
 50 55 60  
 Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser  
 65 70 75 80  
 Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln  
 85 90 95  
 Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser  
 100 105 110  
 Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu  
 115 120 125  
 Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu  
 130 135 140  
 Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr  
 145 150 155 160  
 Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe  
 165 170 175  
 Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro  
 180 185 190  
 Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val  
 195 200 205  
 Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val  
 210 215 220  
 Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser  
 225 230 235 240  
 Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr  
 245 250 255  
 Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly  
 260 265 270  
 Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg  
 275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu  
 290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln  
 305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu  
 325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly  
 340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala  
 355 360 365

Val Val Val Pro Leu Arg Val Glx  
 370 375

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln  
 1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn  
 20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp  
 35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu  
 50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg  
 65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg  
 85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro  
 100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115		120		125
Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe				
130		135		140
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe				
145		150		155
				160
Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg				
		165		170
				175
Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser				
		180		185
				190
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp				
		195		200
				205
Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg				
		210		215
				220
Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg				
		225		230
				235
				240
Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu				
		245		250
				255
Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile				
		260		265
				270
Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn				
		275		280
				285
Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu				
		290		295
				300
Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn				
		305		310
				315
				320
Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val				
		325		330
				335
Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala				
		340		345
				350
Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx				
		355		360
				365

<210> 110  
 <211> 367  
 <212> PRT  
 <213> Proteus mirabilis

<400> 110

Met	Lys	Phe	Ile	Ile	Glu	Arg	Glu	Gln	Leu	Leu	Lys	Pro	Leu	Gln	Gln	1	5	10	15
Val	Ser	Gly	Pro	Leu	Gly	Gly	Arg	Pro	Thr	Leu	Pro	Ile	Leu	Gly	Asn	20	25	30	
Leu	Leu	Leu	Lys	Val	Thr	Glu	Asn	Thr	Leu	Ser	Leu	Thr	Gly	Thr	Asp	35	40	45	
Leu	Glu	Met	Glu	Met	Met	Ala	Arg	Val	Ser	Leu	Ser	Gln	Ser	His	Glu	50	55	60	
Ile	Gly	Ala	Thr	Thr	Val	Pro	Ala	Arg	Lys	Phe	Phe	Asp	Ile	Trp	Arg	65	70	75	80
Gly	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Ser	Val	Glu	Leu	Asp	Gly	Asp	Arg	85	90	95	
Leu	Leu	Val	Arg	Ser	Gly	Arg	Ser	Arg	Phe	Ser	Leu	Ser	Thr	Leu	Pro	100	105	110	
Ala	Ser	Asp	Phe	Pro	Asn	Leu	Asp	Asp	Trp	Gln	Ser	Glu	Val	Glu	Phe	115	120	125	
Thr	Leu	Pro	Gln	Ala	Thr	Leu	Lys	Arg	Leu	Ile	Glu	Ser	Thr	Gln	Phe	130	135	140	
Ser	Met	Ala	His	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Phe	145	150	155	160
Glu	Thr	Glu	Asn	Thr	Glu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg	165	170	175	
Leu	Ala	Val	Cys	Ala	Met	Asp	Ile	Gly	Gln	Ser	Leu	Pro	Gly	His	Ser	180	185	190	
Val	Ile	Val	Pro	Arg	Lys	Gly	Val	Ile	Glu	Leu	Met	Arg	Leu	Leu	Asp	195	200	205	
Gly	Ser	Gly	Glu	Ser	Leu	Leu	Gln	Leu	Gln	Ile	Gly	Ser	Asn	Asn	Leu	210	215	220	

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly  
 225 230 235 240

Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr  
 245 250 255

Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala  
 260 265 270

Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn  
 275 280 285

Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu  
 290 295 300

Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe  
 305 310 315 320

Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu  
 325 330 335

Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn  
 340 345 350

Val Ala Ser Ala Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu  
 355 360 365

<210> 111

<211> 366

<212> PRT

<213> Haemophilus influenzae

<400> 111

Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln  
 1 5 10 15

Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn  
 20 25 30

Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp  
 35 40 45

Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Ser Glu  
 50 55 60

Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg  
 65 70 75 80

Thr Leu Ser Asp Asp Ser Glu Ile Thr Val Thr Phe Glu Gln Asp Arg  
 85 90 95  
 Ala Leu Val Gln Ser Gly Arg Ser Arg Phe Thr Leu Ala Thr Gln Pro  
 100 105 110  
 Ala Glu Glu Tyr Pro Asn Leu Thr Asp Trp Gln Ser Glu Val Asp Phe  
 115 120 125  
 Glu Leu Pro Gln Asn Thr Leu Arg Arg Leu Ile Glu Ala Thr Gln Phe  
 130 135 140  
 Ser Met Ala Asn Gln Asp Ala Arg Tyr Phe Leu Asn Gly Met Lys Phe  
 145 150 155 160  
 Glu Thr Glu Gly Asn Leu Leu Arg Thr Val Ala Thr Asp Gly His Arg  
 165 170 175  
 Leu Ala Val Cys Thr Ile Ser Leu Glu Gln Glu Leu Gln Asn His Ser  
 180 185 190  
 Val Ile Leu Pro Arg Lys Gly Val Leu Glu Leu Val Arg Leu Leu Glu  
 195 200 205  
 Thr Asn Asp Glu Pro Ala Arg Leu Gln Ile Gly Thr Asn Asn Leu Arg  
 210 215 220  
 Val His Leu Lys Asn Thr Val Phe Thr Ser Lys Leu Ile Asp Gly Arg  
 225 230 235 240  
 Phe Pro Asp Tyr Arg Arg Val Leu Pro Arg Asn Ala Thr Lys Ile Val  
 245 250 255  
 Glu Gly Asn Trp Glu Met Leu Lys Gln Ala Phe Ala Arg Ala Ser Ile  
 260 265 270  
 Leu Ser Asn Glu Arg Ala Arg Ser Val Arg Leu Ser Leu Lys Glu Asn  
 275 280 285  
 Gln Leu Lys Ile Thr Ala Ser Asn Thr Glu His Glu Glu Ala Glu Glu  
 290 295 300  
 Ile Val Asp Val Asn Tyr Asn Gly Glu Glu Leu Glu Val Gly Phe Asn  
 305 310 315 320  
 Val Thr Tyr Ile Leu Asp Val Leu Asn Ala Leu Lys Cys Asn Gln Val  
 325 330 335



Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys  
340 345 350

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu  
355 360 365

<210> 112

<211> 367

<212> PRT

<213> Pseudomonas putida

<400> 112

Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu  
1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn  
20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp  
35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu  
50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys  
65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys  
85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro  
100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys  
115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe  
130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu  
145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg  
165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His

180	185	190
Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu		
195	200	205
Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile		
210	215	220
Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly		
225	230	235
Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu		
245	250	255
Val Val Gly Asp Arg Gln Ala Leu Arg Glu Ala Phe Ser Arg Thr Ala		
260	265	270
Ile Leu Ser Asn Glu Lys Tyr Arg Gly Ile Arg Leu Gln Leu Ala Ala		
275	280	285
Gly Gln Leu Lys Ile Gln Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu		
290	295	300
Glu Glu Ile Ser Val Asp Tyr Glu Gly Ser Ser Leu Glu Ile Gly Phe		
305	310	315
Asn Val Ser Tyr Leu Leu Asp Val Leu Gly Val Met Thr Thr Glu Gln		
325	330	335
Val Arg Leu Ile Leu Ser Asp Ser Asn Ser Ser Ala Leu Leu Gln Glu		
340	345	350
Ala Gly Asn Asp Asp Ser Ser Tyr Val Val Met Pro Met Arg Leu		
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<210> 113  
 <211> 366  
 <212> PRT  
 <213> Buchnera aphidicola

<400> 113  
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Ile Leu Ile Gln Val Glu Asp Gly Thr Leu Ser Leu Thr Thr Thr Asn  
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 Leu Glu Ile Glu Leu Ile Ser Lys Ile Glu Ile Ile Thr Lys Tyr Ile  
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 Pro Gly Lys Thr Thr Ile Ser Gly Arg Lys Ile Leu Asn Ile Cys Arg  
 65 70 75 80  
 Thr Leu Ser Glu Lys Ser Lys Ile Lys Met Gln Leu Lys Asn Lys Lys  
 85 90 95  
 Met Tyr Ile Ser Ser Glu Asn Ser Asn Tyr Ile Leu Ser Thr Leu Ser  
 100 105 110  
 Ala Asp Thr Phe Pro Asn His Gln Asn Phe Asp Tyr Ile Ser Lys Phe  
 115 120 125  
 Asp Ile Ser Ser Asn Ile Leu Lys Glu Met Ile Glu Lys Thr Glu Phe  
 130 135 140  
 Ser Met Gly Lys Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu  
 145 150 155 160  
 Glu Lys Lys Asp Lys Phe Leu Arg Ser Val Ala Thr Asp Gly Tyr Arg  
 165 170 175  
 Leu Ala Ile Ser Tyr Thr Gln Leu Lys Lys Asp Ile Asn Phe Phe Ser  
 180 185 190  
 Ile Ile Ile Pro Asn Lys Ala Val Met Glu Leu Leu Lys Leu Leu Asn  
 195 200 205  
 Thr Gln Pro Gln Leu Leu Asn Ile Leu Ile Gly Ser Asn Ser Ile Arg  
 210 215 220  
 Ile Tyr Thr Lys Asn Leu Ile Phe Thr Thr Gln Leu Ile Glu Gly Glu  
 225 230 235 240  
 Tyr Pro Asp Tyr Lys Ser Val Leu Phe Lys Glu Lys Lys Asn Pro Ile  
 245 250 255  
 Ile Thr Asn Ser Ile Leu Leu Lys Lys Ser Leu Leu Arg Val Ala Ile  
 260 265 270  
 Leu Ala His Glu Lys Phe Cys Gly Ile Glu Ile Lys Ile Glu Asn Gly  
 275 280 285

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp  
 290 295 300

Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn  
 305 310 315 320

Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile  
 325 330 335

Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu  
 340 345 350

Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg  
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<210> 114

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 114

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<210> 115

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 115

gtgtggatcc gtggtgacct tagccac 27

<210> 116

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 116

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30

<210> 117

<211> 3514

<212> DNA

<213> *Aquifex aeolicus*

<400> 117

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attaagccca taatcggcat ggaagcctac tttaccacgg gttcgagggt tgacagaaaag 240
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gtaagaagaa agcggattta atggctcaga tgaaagacaa gttcatacag ggagcgggtg 2280
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<210> 118

<211> 1161

<212> PRT

<213> Aquifex aeolicus

<400> 118

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Met Ser Lys Asp Phe Val His Leu His Leu His Thr Gln Phe Ser Leu
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Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu
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Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly
      35                   40                   45

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
      50                   55                   60

Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
      65                   70                   75                   80

Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
      85                   90                   95

Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu

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Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala		
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Cys Leu Lys Gly Val Pro Thr Tyr Tyr Ala Ser Ile Asn Glu Val Lys		
145	150	155
Lys Ala Glu Glu Trp Val Lys Lys Phe Lys Asp Ile Phe Gly Asp Asp		
165	170	175
Leu Tyr Leu Glu Leu Gln Ala Asn Asn Ile Pro Glu Gln Glu Val Ala		
180	185	190
Asn Arg Asn Leu Ile Glu Ile Ala Lys Lys Tyr Asp Val Lys Leu Ile		
195	200	205
Ala Thr Gln Asp Ala His Tyr Leu Asn Pro Glu Asp Arg Tyr Ala His		
210	215	220
Thr Val Leu Met Ala Leu Gln Met Lys Lys Thr Ile His Glu Leu Ser		
225	230	235
Ser Gly Asn Phe Lys Cys Ser Asn Glu Asp Leu His Phe Ala Pro Pro		
245	250	255
Glu Tyr Met Trp Lys Lys Phe Glu Gly Lys Phe Glu Gly Trp Glu Lys		
260	265	270
Ala Leu Leu Asn Thr Leu Glu Val Met Glu Lys Thr Ala Asp Ser Phe		
275	280	285
Glu Ile Phe Glu Asn Ser Thr Tyr Leu Leu Pro Lys Tyr Asp Val Pro		
290	295	300
Pro Asp Lys Thr Leu Glu Glu Tyr Leu Arg Glu Leu Ala Tyr Lys Gly		
305	310	315
Leu Arg Gln Arg Ile Glu Arg Gly Gln Ala Lys Asp Thr Lys Glu Tyr		
325	330	335
Trp Glu Arg Leu Glu Tyr Glu Leu Glu Val Ile Asn Lys Met Gly Phe		
340	345	350
Ala Gly Tyr Phe Leu Ile Val Gln Asp Phe Ile Asn Trp Ala Lys Lys		

355		360		365
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370		375		380
Val Ala Tyr Ala Ile Gly Ile Thr Asp Val Asp Pro Ile Lys His Gly				
385		390		395
				400
Phe Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp				
	405		410	415
Ile Asp Val Asp Phe Cys Gln Asp Asn Arg Glu Lys Val Ile Glu Tyr				
	420		425	430
Val Arg Asn Lys Tyr Gly His Asp Asn Val Ala Gln Ile Ile Thr Tyr				
	435		440	445
Asn Val Met Lys Ala Lys Gln Thr Leu Arg Asp Val Ala Arg Ala Met				
	450		455	460
Gly Leu Pro Tyr Ser Thr Ala Asp Lys Leu Ala Lys Leu Ile Pro Gln				
465		470		475
				480
Gly Asp Val Gln Gly Thr Trp Leu Ser Leu Glu Glu Met Tyr Lys Thr				
	485		490	495
Pro Val Glu Glu Leu Leu Gln Lys Tyr Gly Glu His Arg Thr Asp Ile				
	500		505	510
Glu Asp Asn Val Lys Lys Phe Arg Gln Ile Cys Glu Glu Ser Pro Glu				
	515		520	525
Ile Lys Gln Leu Val Glu Thr Ala Leu Lys Leu Glu Gly Leu Thr Arg				
	530		535	540
His Thr Ser Leu His Ala Ala Gly Val Val Ile Ala Pro Lys Pro Leu				
545		550		555
				560
Ser Glu Leu Val Pro Leu Tyr Tyr Asp Lys Glu Gly Glu Val Ala Thr				
	565		570	575
Gln Tyr Asp Met Val Gln Leu Glu Glu Leu Gly Leu Leu Lys Met Asp				
	580		585	590
Phe Leu Gly Leu Lys Thr Leu Thr Glu Leu Lys Leu Met Lys Glu Leu				
	595		600	605
Ile Lys Glu Arg His Gly Val Asp Ile Asn Phe Leu Glu Leu Pro Leu				



610	615	620
Asp Asp Pro Lys Val Tyr Lys Leu Leu Gln Glu Gly Lys Thr Thr Gly		
625	630	635 640
Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu		
	645	650 655
Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg		
	660	665 670
Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys		
	675	680 685
His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val		
	690	695 700
Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys		
705	710	715 720
Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu		
	725	730 735
Arg Lys Ala Ile Gly Lys Lys Lys Ala Asp Leu Met Ala Gln Met Lys		
	740	745 750
Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys		
	755	760 765
Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe		
	770	775 780
Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala		
785	790	795 800
Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr		
	805	810 815
Thr Glu Lys Asn Asp Asn Lys Phe Leu Asn Leu Ile Lys Asp Ala Lys		
	820	825 830
Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val		
	835	840 845
Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg		
850	855	860
Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg		

865		870		875		880
Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr						
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Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala						
	900		905		910	
Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys						
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Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe						
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Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu						
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Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr						
	965		970		975	
Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu						
	980		985		990	
Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu						
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Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu						
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Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr						
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Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Val Lys						
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Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val						
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Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr						
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Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu						
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Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn						
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Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu						

1125

1130

1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile

1140

1145

1150

Glu Lys Leu Gly Val Lys Val Ile Ile

1155

1160

&lt;210&gt; 119

&lt;211&gt; 2408

&lt;212&gt; DNA

&lt;213&gt; Aquifex aeolicus

&lt;400&gt; 119

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2408

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 <212> PRT  
 <213> Aquifex aeolicus

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 Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly  
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 Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys  
 50 55 60  
 Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg  
 65 70 75 80  
 Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala  
 85 90 95  
 Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn  
 100 105 110  
 Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala  
 115 120 125  
 His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu  
 130 135 140  
 Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp  
 145 150 155 160  
 Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser  
 165 170 175

Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu  
 180 185 190  
 Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His  
 195 200 205  
 Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala  
 210 215 220  
 Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe  
 225 230 235 240  
 Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu  
 245 250 255  
 Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser  
 260 265 270  
 Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu  
 275 280 285  
 Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val  
 290 295 300  
 Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu  
 305 310 315 320  
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 325 330 335  
 Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser  
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 Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val  
 355 360 365  
 Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro  
 370 375 380  
 Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln  
 385 390 395 400  
 Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu  
 405 410 415  
 Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu  
 420 425 430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu  
 435 440 445

Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro  
 450 455 460

Gln Lys Ser Ser Gly Thr Arg Leu Phe  
 465 470

<210> 121  
 <211> 1090  
 <212> DNA  
 <213> Aquifex aeolicus

<400> 121  
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 aacttaatcg taagggcaac ggacttggaa aactaccttg tagtctccgt aaagggggag 180  
 gttgaagagg aaggagaggt ttgctccac tctcaaaaac tctacgatag agtcaagaac 240  
 ttaaattccg cttacgttta ccttcatacg gaaggtgaaa aactcgtcat aacgggagga 300  
 aagagtacgt acaaacttcc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360  
 gtagaaggag gagaaacact ttcgggaaac cttctcgtta acggaataga aaaggtagag 420  
 tacgccatag cgaaggaaga agcgaacata gcccttcagg gaatgtatct gagaggatac 480  
 gaggacagaa ttcactttgt gttcggacgg tcacaggctt gcactttatg aacctctacg 540  
 taaacattga aaagagtga gacgagtctt ttgcttactt ctccactccc gagtggaaac 600  
 tcgccgttag ctcttggaag gagaattccc ggactacatg agtgtcatcc ctgaggagtt 660  
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 tgagttcgcg gatccggagt tcggagaagc gagagaggaa attgaagtgg agtacacggg 840  
 agagcccttt gagataggat tcaacggaaa taccttatgg aggcgcttga cgcctacgac 900  
 agcgaaagag tgtggttcaa gttcacaacc cccgacacgg ccactttatt ggaggctgaa 960  
 gattacgaaa aggaacctta caagtgcata ataatgccga tgaggggtgta gccatgaaaa 1020  
 aagctttaat ctttttattg agcttgagcc ttttaattcc tgcgttttagc gaagccaaac 1080  
 ccaagtcttc 1090

<210> 122  
 <211> 363  
 <212> PRT  
 <213> Aquifex aeolicus

<400> 122  
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Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn

20	25	30
Phe Leu Leu Ser Ala Lys Glu Glu Asn Leu Ile Val Arg Ala Thr Asp		
35	40	45
Leu Glu Asn Tyr Leu Val Val Ser Val Lys Gly Glu Val Glu Glu Glu		
50	55	60
Gly Glu Val Cys Val His Ser Gln Lys Leu Tyr Asp Ile Val Lys Asn		
65	70	75
		80
Leu Asn Ser Ala Tyr Val Tyr Leu His Thr Glu Gly Glu Lys Leu Val		
	85	90
		95
Ile Thr Gly Gly Lys Ser Thr Tyr Lys Leu Pro Thr Ala Pro Ala Glu		
100	105	110
Asp Phe Pro Glu Phe Pro Glu Ile Val Glu Gly Gly Glu Thr Leu Ser		
115	120	125
Gly Asn Leu Leu Val Asn Gly Ile Glu Lys Val Glu Tyr Ala Ile Ala		
130	135	140
Lys Glu Glu Ala Asn Ile Ala Leu Gln Gly Met Tyr Leu Arg Gly Tyr		
145	150	155
		160
Glu Asp Arg Ile His Phe Val Gly Ser Asp Gly His Arg Leu Ala Leu		
	165	170
		175
Tyr Glu Pro Leu Gly Glu Phe Ser Lys Glu Leu Leu Ile Pro Arg Lys		
180	185	190
Ser Leu Lys Val Leu Lys Lys Leu Ile Thr Gly Ile Glu Asp Val Asn		
195	200	205
Ile Glu Lys Ser Glu Asp Glu Ser Phe Ala Tyr Phe Ser Thr Pro Glu		
210	215	220
Trp Lys Leu Ala Val Arg Leu Leu Glu Gly Glu Phe Pro Asp Tyr Met		
225	230	235
		240
Ser Val Ile Pro Glu Glu Phe Ser Ala Glu Val Leu Phe Glu Thr Glu		
	245	250
		255
Glu Val Leu Lys Val Leu Lys Arg Leu Lys Ala Leu Ser Glu Gly Lys		
260	265	270
Val Phe Pro Val Lys Ile Thr Leu Ser Glu Asn Leu Ala Ile Phe Glu		

275                                      280                                      285  
 Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu  
 290                                      295                                      300  
 Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met  
 305                                      310                                      315                                      320  
 Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr  
 325                                      330                                      335  
 Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu  
 340                                      345                                      350  
 Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val  
 355                                      360

<210> 123  
 <211> 1093  
 <212> DNA  
 <213> Aquifex aeolicus

<400> 123  
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 gaaaagtacg gggagaatta cacgggttctg tgggggggatg agataagcga ggaggaattc 180  
 tacactgccc tttccgagac cagtatatctt ggcgggttcaa aggaaaaagc ggtgggtcatt 240  
 tacaacttcg gggatttcct gaagaagctc ggaaggaaga aaaaggaaaa agaaaggctt 300  
 ataaaagtcc tcagaaacgt aaagagtaac tacgtattta tagtgtacga tgcgaaactc 360  
 cagaaacagg aactttcttc ggaacctctg aaatccgtag cgtctttcgg cggatatagt 420  
 gtagcaaaca ggctgagcaa ggagaggata aaacagctcg tccttaagaa gttcaaagaa 480  
 aaagggataa acgtagaaaa cgatgccctt gaataccttc tccagctcac gggttacaac 540  
 ttgatggagc tcaaacttga ggttgaaaaa ctgatagatt acgcaagtga aaagaaaatt 600  
 ttaacactcg atgaggtaaa gagagtagcc ttctcagtct cagaaaacgt aaacgtattt 660  
 gagttcgttg atttactcct cttaaaagat tacgaaaagg ctcttaaagt tttggactcc 720  
 ctcatcttct tcggaatata cccctccag attatgaaaa tcctgtcctc ctatgctcta 780  
 aaactttaca ccctcaagag gcttgaagag aaggggagagg acctgaataa ggcgatggaa 840  
 agcgtgggaa taaagaacaa ctttctcaag atgaagttca aatcttactt aaaggcaaac 900  
 tctaaagagg acttgaagaa cctaatacctc tccctccaga ggatagacgc tttttctaaa 960  
 ctttactttc aggacacagt gcagttgctg gggatttctt gacctcaaga ctggagaggg 1020  
 aagttgtgaa aaatacttct catggtggat aatctttttt atgaagtttg cggtttgcgt 1080  
 ttttcccggt tct 1093

<210> 124  
 <211> 350  
 <212> PRT



<213> Aquifex aeolicus

<400> 124

Val	Glu	Thr	Thr	Ile	Phe	Gln	Phe	Gln	Lys	Thr	Phe	Phe	Thr	Lys	Pro	
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Pro	Lys	Glu	Arg	Val	Phe	Val	Leu	His	Gly	Glu	Glu	Gln	Tyr	Leu	Ile	
			20					25					30			
Arg	Thr	Phe	Leu	Ser	Lys	Leu	Lys	Glu	Lys	Tyr	Gly	Glu	Asn	Tyr	Thr	
		35					40					45				
Val	Leu	Trp	Gly	Asp	Glu	Ile	Ser	Glu	Glu	Glu	Phe	Tyr	Thr	Ala	Leu	
	50					55					60					
Ser	Glu	Thr	Ser	Ile	Phe	Gly	Gly	Ser	Lys	Glu	Lys	Ala	Val	Val	Ile	
65				70						75					80	
Tyr	Asn	Phe	Gly	Asp	Phe	Leu	Lys	Lys	Leu	Gly	Arg	Lys	Lys	Lys	Glu	
				85					90						95	
Lys	Glu	Arg	Leu	Ile	Lys	Val	Leu	Arg	Asn	Val	Lys	Ser	Asn	Tyr	Val	
		100						105					110			
Phe	Ile	Val	Tyr	Asp	Ala	Lys	Leu	Gln	Lys	Gln	Glu	Leu	Ser	Ser	Glu	
		115					120					125				
Pro	Leu	Lys	Ser	Val	Ala	Ser	Phe	Gly	Gly	Ile	Val	Val	Ala	Asn	Arg	
	130					135					140					
Leu	Ser	Lys	Glu	Arg	Ile	Lys	Gln	Leu	Val	Leu	Lys	Lys	Phe	Lys	Glu	
145				150						155					160	
Lys	Gly	Ile	Asn	Val	Glu	Asn	Asp	Ala	Leu	Glu	Tyr	Leu	Leu	Gln	Leu	
			165						170					175		
Thr	Gly	Tyr	Asn	Leu	Met	Glu	Leu	Lys	Leu	Glu	Val	Glu	Lys	Leu	Ile	
		180						185					190			
Asp	Tyr	Ala	Ser	Glu	Lys	Lys	Ile	Leu	Thr	Leu	Asp	Glu	Val	Lys	Arg	
	195						200					205				
Val	Ala	Phe	Ser	Val	Ser	Glu	Asn	Val	Asn	Val	Phe	Glu	Phe	Val	Asp	
	210					215					220					
Leu	Leu	Leu	Leu	Lys	Asp	Tyr	Glu	Lys	Ala	Leu	Lys	Val	Leu	Asp	Ser	
225				230						235					240	

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser  
245 250 255

Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly  
260 265 270

Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe  
275 280 285

Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp  
290 295 300

Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys  
305 310 315 320

Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser  
325 330 335

Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly  
340 345 350

<210> 125

<211> 1051

<212> DNA

<213> Aquifex aeolicus

<400> 125

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ttatgtaagg aaaacgtacc tggggatgcg gaagtgtgcc ctctgcaaa cacgtaaacg 180
agctggagga agccttcttt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
cggtaaaaaag cacttcgttt accttatggg cgaacatccc gactttgtgg taataatccc 300
gagcggacat tacataaaga tagaacagat aagggaagtt aagaactttg cctatgtgaa 360
gcccgacta agcaggagaa aagtaattat aatagacgac gccacgcga tgacctctca 420
ggcggcaaac gctcttttaa aggtattgga agagccacct gcggacacca cttttatctt 480
gaccacgaac aggcgttctg caatcctgcc gactatcctc tccagaactt ttcaagtgga 540
gttcaagggc ttttcagtaa aagaggttat ggaaatagcg aaagtagacg aggaaatagc 600
gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaca aagatattct 660
aaacaaagta aaggaattct tggaaaacga gccgttaaaa gtttacaagc ttgcaagtga 720
attcgaaaag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattggt 780
atctcaaaaa ttgaccgaag agaaaaaaga caattacacc taccttcttg atacgatcag 840
actcttttaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900
cggttcaggcg gattaataaa ccgttattga ttccgtaaca tttaaacctt aatctaaatt 960
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ggaagatagg aaccgtgagc ggtgtaaaag t
1051

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<210> 126  
 <211> 305  
 <212> PRT  
 <213> Aquifex aeolicus

<400> 126

Met	Glu	Lys	Val	Phe	Leu	Glu	Lys	Leu	Gln	Lys	Thr	Leu	His	Ile	Pro
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Gly	Gly	Leu	Leu	Phe	Tyr	Gly	Lys	Glu	Gly	Ser	Gly	Lys	Thr	Lys	Thr
			20					25					30		
Ala	Phe	Glu	Phe	Ala	Lys	Gly	Ile	Leu	Cys	Lys	Glu	Asn	Val	Pro	Trp
		35					40					45			
Gly	Cys	Gly	Ser	Cys	Pro	Ser	Cys	Lys	His	Val	Asn	Glu	Leu	Glu	Glu
	50					55					60				
Ala	Phe	Phe	Lys	Gly	Glu	Ile	Glu	Asp	Phe	Lys	Val	Tyr	Lys	Asp	Lys
65					70					75					80
Asp	Gly	Lys	Lys	His	Phe	Val	Tyr	Leu	Met	Gly	Glu	His	Pro	Asp	Phe
				85					90					95	
Val	Val	Ile	Ile	Pro	Ser	Gly	His	Tyr	Ile	Lys	Ile	Glu	Gln	Ile	Arg
			100					105					110		
Glu	Val	Lys	Asn	Phe	Ala	Tyr	Val	Lys	Pro	Ala	Leu	Ser	Arg	Arg	Lys
		115					120					125			
Val	Ile	Ile	Ile	Asp	Asp	Ala	His	Ala	Met	Thr	Ser	Gln	Ala	Ala	Asn
	130					135					140				
Ala	Leu	Leu	Lys	Val	Leu	Glu	Glu	Pro	Pro	Ala	Asp	Thr	Thr	Phe	Ile
145					150					155					160
Leu	Thr	Thr	Asn	Arg	Arg	Ser	Ala	Ile	Leu	Pro	Thr	Ile	Leu	Ser	Arg
			165					170						175	
Thr	Phe	Gln	Val	Glu	Phe	Lys	Gly	Phe	Ser	Val	Lys	Glu	Val	Met	Glu
		180					185						190		
Ile	Ala	Lys	Val	Asp	Glu	Glu	Ile	Ala	Lys	Leu	Ser	Gly	Gly	Ser	Leu
		195					200					205			
Lys	Arg	Ala	Ile	Leu	Leu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	Asn	Lys	Val
	210					215					220				

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser  
 225 230 235 240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile  
 245 250 255

Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn  
 260 265 270

Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala  
 275 280 285

Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala  
 290 295 300

Asp  
 305

<210> 127  
 <211> 630  
 <212> DNA  
 <213> Aquifex aeolicus

<400> 127  
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 gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tcctttcaat aggtgcggtt 180  
 gaggttaaaa acctggaaat agacctctct aaatcttttt acgagatact caaaagtgc 240  
 gagataaagg cggcggagat acatggaata accagggaag acgttgaaaa gtacggaaag 300  
 gaaccaaagg aagtaataata cgactttctg aagtacataa agggaagcgt tctcgttggc 360  
 tactacgtga agtttgacgt ctactcgtt gagaagtact ccataaagta cttccagtat 420  
 ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480  
 aggagtcttg acgaccttat gaaggaaactc ggtgtagaaa taagggaag gcacaacgcc 540  
 cttgaagatg cctacataac cgctcttctt ttcctaaagt acgtttaccc gaacaggagg 600  
 tacagactaa aggatctccc gattttcctt 630

<210> 128  
 <211> 210  
 <212> PRT  
 <213> Aquifex aeolicus

<400> 128  
 Met Asn Phe Leu Lys Lys Phe Leu Leu Leu Arg Lys Ala Gln Lys Ser  
 1 5 10 15  
 Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val

20	25	30
Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp		
35	40	45
Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn		
50	55	60
Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp		
65	70	75 80
Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu		
85	90	95
Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr		
100	105	110
Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser		
115	120	125
Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn		
130	135	140
Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly		
145	150	155 160
Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala		
165	170	175
Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu		
180	185	190
Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile		
195	200	205
Phe Leu		
210		

<210> 129  
 <211> 526  
 <212> DNA  
 <213> Aquifex aeolicus

<400> 129  
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 ccgagcggaa cgcccgtagt agagtttact ctggcttaca acagaaggta taaaaccag 120  
 aacggtgaat ttcaggagga aagtcacttc tttgacgtaa aggcgtacgg aaaaatggct 180

gaagactggg ctacacgctt ctcgaaagga tacctcgtag tcgtagaggg aagactctcc 240  
caggaaaagt gggagaaaga aggaaagaag ttctcaaagg tcaggataat agcggaaaac 300  
gtaagattaa taaacaggcc gaaagggtgct gaacttcaag cagaagaaga ggaggaagtt 360  
cctcccattg aggaggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420  
gaagaggacg aaataccttt ttaattttga ggagggttaa gtatggtagt gagagctcct 480  
aagaagaaag tttgtatgta ctgtgaacaa aagagagagc cagatt 526

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val  
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Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala  
20 25 30

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser  
35 40 45

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala  
50 55 60

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser  
65 70 75 80

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile  
85 90 95

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu  
100 105 110

Gln Ala Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu  
115 120 125

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu  
130 135 140

Ile Pro Phe  
145

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

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aataagctcg atttcgtatt aataaaggat caccttgaaa agaaaaactt actccagaaa 240
atacctatag actggctcga agaactctac gaggaggcgg tatcccctga cacgcttgag 300
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ttaataatac tcgccgcaag acccggtatg gggaaaaccg cctttatgct ctccataatc 660
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gaacagctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataagg 780
tctggaagta tatcgaatga agatttaaag aagcttgaag caagcgcaat agaactcgca 840
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gaggtggaaa agaggagtga taaaagaccc cagcttgcgg acctcagaga atccggacag 1140
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gaaggattcg aagatattga cttctgaaaa ttaaggtttt ataattttat cttggctatc 1440
cggggtagct caatcggcag agcgggtggc tg 1472
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<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

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Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
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Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
          20                      25                      30

Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
          35                      40                      45

Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
          50                      55                      60
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Phe Val Leu Ile Lys Asp His Leu Glu Lys Lys Asn Leu Leu Gln Lys  
65 70 75 80

Ile Pro Ile Asp Trp Leu Glu Glu Leu Tyr Glu Glu Ala Val Ser Pro  
85 90 95

Asp Thr Leu Glu Glu Val Cys Lys Ile Val Lys Gln Arg Ser Ala Gln  
100 105 110

Arg Ala Ile Ile Gln Leu Gly Ile Thr Ser Thr Gln Phe Tyr His Val  
115 120 125

Lys Asp Val Ala Glu Glu Val Ile Glu Leu Ile Tyr Lys Phe Lys Ser  
130 135 140

Ser Asp Arg Leu Val Thr Gly Leu Pro Ser Gly Phe Thr Glu Leu Asp  
145 150 155 160

Leu Lys Thr Thr Gly Phe His Pro Gly Asp Leu Ile Ile Leu Ala Ala  
165 170 175

Arg Pro Gly Met Gly Lys Thr Ala Phe Met Leu Ser Ile Ile Tyr Asn  
180 185 190

Leu Ala Lys Asp Glu Gly Lys Pro Ser Ala Val Phe Ser Leu Glu Met  
195 200 205

Ser Lys Glu Gln Leu Val Met Arg Leu Leu Ser Met Met Ser Glu Val  
210 215 220

Pro Leu Phe Lys Ile Arg Ser Gly Ser Ile Ser Asn Glu Asp Leu Lys  
225 230 235 240

Lys Leu Glu Ala Ser Ala Ile Glu Leu Ala Lys Tyr Asp Ile Tyr Leu  
245 250 255

Asp Asp Thr Pro Ala Leu Thr Thr Thr Asp Leu Arg Ile Arg Ala Arg  
260 265 270

Lys Leu Arg Lys Glu Lys Glu Val Glu Phe Val Ala Val Asp Tyr Leu  
275 280 285

Gln Leu Leu Arg Pro Pro Val Arg Lys Ser Ser Arg Gln Glu Glu Val  
290 295 300

Ala Glu Val Ser Arg Asn Leu Lys Ala Leu Ala Lys Glu Leu His Ile  
305 310 315 320



Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser  
325 330 335

Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu  
340 345 350

Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys  
355 360 365

Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala  
370 375 380

Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys  
385 390 395 400

Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro  
405 410 415

Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly  
420 425 430

Phe Glu Asp Ile Asp Phe  
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<210> 133

<211> 1526

<212> DNA

<213> Aquifex aeolicus

<400> 133

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gatacacccct ccttttacgt gtctccaagt aaacaaatat tcaagtgttt cggttgcggg 180
gtaggggggag acgcgataaa gttcgtttcc ctttacgagg acatctccta ttttgaagcc 240
gcccttgaac tcgcaaaacg ctacggaaag aaattagacc ttgaaaagat atcaaaagac 300
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aacagagagg caagtgahta cgtaaagagt aggggaatag accctaaagt agcgaggaag 420
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gatctctttc ttcggcgtgt cgtgatcccg ataaaggatc cgaggggaag agttataggt 600
ttcggtgga ggaggatagt agaggacaaa tctcccaagt acataaactc tccagacagc 660
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gaagaaggat ttgcgatact tgtggaaggg tactttgacc ttttgagact tttttccgag 780
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gctatgaaaa gtgccattcc cctactcctc agtgcaggag tggaagttaa tcccgtttac 960
ctccccgaag gatacgatcc cgacgagttt ataaaggaat tcgggaaaga ggaattaaga 1020
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gaagtctcg agtaccaggt ggataacttg gagaaacttt ttaacaacat ccttagggat 1440
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actttaataa atttttagag ttagga                                     1526

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<210> 134  
 <211> 498  
 <212> PRT  
 <213> Aquifex aeolicus

<400> 134

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Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
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Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
      35             40            45

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
      50             55            60

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
      65             70            75            80

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
      85             90            95

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
      100            105           110

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
      115            120           125

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
      130            135           140

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
      145            150           155           160

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys

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	165		170		175
Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys					
	180		185		190
Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu					
	195		200		205
Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys					
	210		215		220
Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys					
	225		230		235
Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg					
	245		250		255
Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala					
	260		265		270
Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val					
	275		280		285
Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser					
	290		295		300
Ala Ile Pro Leu Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr					
	305		310		315
Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys					
	325		330		335
Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr					
	340		345		350
Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe					
	355		360		365
Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu					
	370		375		380
Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu					
	385		390		395
Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe					
	405		410		415
Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile					

420                                      425                                      430  
 Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val  
           435                                      440                                      445  
 Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu  
           450                                      455                                      460  
 Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp  
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 Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val  
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 Asn Thr

<210> 135  
 <211> 705  
 <212> DNA  
 <213> Aquifex aeolicus

<400> 135  
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 atcccaaaga ggtactggaa cgccaactta gacacttacc accccaagaa cgtatcccag 180  
 aacagggcac ttttgacgat aaggggtcttc gtccacaact tcaatcccga ggaagggaaa 240  
 gggcttacct ttgtaggatc tcttggagtc ggcaaaactc accttgcggt tgcaacatta 300  
 aaagcgattt atgagaagaa gggaatcaga ggatacttct tcgatacgaa ggatctaata 360  
 ttcaggttaa aacacttaat ggacgagggg aaggatacaa agttttttaa aactgtctta 420  
 aactcacggg ttttggttct cgacgacctc ggttctgaga ggctcagtga ctggcagagg 480  
 gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540  
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<210> 136  
 <211> 235  
 <212> PRT  
 <213> Aquifex aeolicus

<400> 136  
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 Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys

20	25	30
Arg Asp Val Asn Arg Glu Leu Asn Ile Pro Lys Arg Tyr Trp Asn Ala		
35	40	45
Asn Leu Asp Thr Tyr His Pro Lys Asn Val Ser Gln Asn Arg Ala Leu		
50	55	60
Leu Thr Ile Arg Val Phe Val His Asn Phe Asn Pro Glu Glu Gly Lys		
65	70	75
		80
Gly Leu Thr Phe Val Gly Ser Pro Gly Val Gly Lys Thr His Leu Ala		
85	90	95
Val Ala Thr Leu Lys Ala Ile Tyr Glu Lys Lys Gly Ile Arg Gly Tyr		
100	105	110
Phe Phe Asp Thr Lys Asp Leu Ile Phe Arg Leu Lys His Leu Met Asp		
115	120	125
Glu Gly Lys Asp Thr Lys Phe Leu Lys Thr Val Leu Asn Ser Pro Val		
130	135	140
Leu Val Leu Asp Asp Leu Gly Ser Glu Arg Leu Ser Asp Trp Gln Arg		
145	150	155
		160
Glu Leu Ile Ser Tyr Ile Ile Thr Tyr Arg Tyr Asn Asn Leu Lys Ser		
165	170	175
Thr Ile Ile Thr Thr Asn Tyr Ser Leu Gln Arg Glu Glu Glu Ser Ser		
180	185	190
Val Arg Ile Ser Ala Asp Leu Ala Ser Arg Leu Gly Glu Asn Val Val		
195	200	205
Ser Lys Ile Tyr Glu Met Asn Glu Leu Leu Val Ile Lys Gly Ser Asp		
210	215	220
Leu Arg Lys Ser Lys Lys Leu Ser Thr Pro Ser		
225	230	235

<210> 137

<211> 4101

<212> DNA

<213> *Thermatoga maritima*

<400> 137

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aacggggatc	taaggggaaa	gatactttcc	cttctcaacg	gtaatgtgcc	ttacataaaa	240
gatgttggtt	tcgaaggaaa	caggctgatt	ctgaaagtgc	ttggagattt	cgcgcgggac	300
aggatcgctt	ccaaactcag	aagcacgaaa	aaacagctcg	atgaactgct	gcctcccgga	360
acagagatca	tgctggaggt	tgtggagcct	ccggaagatc	ttttgaaaaa	ggaagtacca	420
caaccagaaa	agagagaaga	accaaagggg	gaagaattga	agatcgagga	tgaaaaccac	480
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gtccttctga	tttacctgac	agacggagaa	gattctctga	tctgcaaagt	cttcaacgac	660
gttgaaaagg	tcgaagggaa	agtatcggtg	ggagacgtga	tcgttgccac	aggagacctc	720
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ctcgacttcg	agacgacggg	tctcgacccg	caggtggatg	agatcatcga	gataggagcg	1140
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4101

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<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

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Met Lys Lys Ile Glu Asn Leu Lys Trp Lys Asn Val Ser Phe Lys Ser
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```

```

Leu Glu Ile Asp Pro Asp Ala Gly Val Val Leu Val Ser Val Glu Lys
      20                      25                      30

```

```

Phe Ser Glu Glu Ile Glu Asp Leu Val Arg Leu Leu Glu Lys Lys Thr
      35                      40                      45

```

```

Arg Phe Arg Val Ile Val Asn Gly Val Gln Lys Ser Asn Gly Asp Leu
      50                      55                      60

```

```

Arg Gly Lys Ile Leu Ser Leu Leu Asn Gly Asn Val Pro Tyr Ile Lys
      65                      70                      75                      80

```

```

Asp Val Val Phe Glu Gly Asn Arg Leu Ile Leu Lys Val Leu Gly Asp
      85                      90                      95

```

```

Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Lys Gln

```

100	105	110
Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val		
115	120	125
Glu Pro Pro Glu Asp Leu Leu Lys Lys Glu Val Pro Gln Pro Glu Lys		
130	135	140
Arg Glu Glu Pro Lys Gly Glu Glu Leu Lys Ile Glu Asp Glu Asn His		
145	150	155
Ile Phe Gly Gln Lys Pro Arg Lys Ile Val Phe Thr Pro Ser Lys Ile		
	165	170
		175
Phe Glu Tyr Asn Lys Lys Thr Ser Val Lys Gly Lys Ile Phe Lys Ile		
	180	185
		190
Glu Lys Ile Glu Gly Lys Arg Thr Val Leu Leu Ile Tyr Leu Thr Asp		
	195	200
		205
Gly Glu Asp Ser Leu Ile Cys Lys Val Phe Asn Asp Val Glu Lys Val		
	210	215
		220
Glu Gly Lys Val Ser Val Gly Asp Val Ile Val Ala Thr Gly Asp Leu		
	225	230
		235
		240
Leu Leu Glu Asn Gly Glu Pro Thr Leu Tyr Val Lys Gly Ile Thr Lys		
	245	250
		255
Leu Pro Glu Ala Lys Arg Met Asp Lys Ser Pro Val Lys Arg Val Glu		
	260	265
		270
Leu His Ala His Thr Lys Phe Ser Asp Gln Asp Ala Ile Thr Asp Val		
	275	280
		285
Asn Glu Tyr Val Lys Arg Ala Lys Glu Trp Gly Phe Pro Ala Ile Ala		
	290	295
		300
Leu Thr Asp His Gly Asn Val Gln Ala Ile Pro Tyr Phe Tyr Asp Ala		
	305	310
		315
		320
Ala Lys Glu Ala Gly Ile Lys Pro Ile Phe Gly Ile Glu Ala Tyr Leu		
	325	330
		335
Val Ser Asp Val Glu Pro Val Ile Arg Asn Leu Ser Asp Asp Ser Thr		
	340	345
		350
Phe Gly Asp Ala Thr Phe Val Val Leu Asp Phe Glu Thr Thr Gly Leu		



355	360	365
Asp Pro Gln Val Asp Glu Ile Ile Glu Ile Gly Ala Val Lys Ile Gln		
370	375	380
Gly Gly Gln Ile Val Asp Glu Tyr His Thr Leu Ile Lys Pro Ser Arg		
385	390	400
Glu Ile Ser Arg Lys Ser Ser Glu Ile Thr Gly Ile Thr Gln Glu Met		
	405	410 415
Leu Glu Asn Lys Arg Ser Ile Glu Glu Val Leu Pro Glu Phe Leu Gly		
	420	425 430
Phe Leu Glu Asp Ser Ile Ile Val Ala His Asn Ala Asn Phe Asp Tyr		
	435	440 445
Arg Phe Leu Arg Leu Trp Ile Lys Lys Val Met Gly Leu Asp Trp Glu		
	450	455 460
Arg Pro Tyr Ile Asp Thr Leu Ala Leu Ala Lys Ser Leu Leu Lys Leu		
465	470	475 480
Arg Ser Tyr Ser Leu Asp Ser Val Val Glu Lys Leu Gly Leu Gly Pro		
	485	490 495
Phe Arg His His Arg Ala Leu Asp Asp Ala Arg Val Thr Ala Gln Val		
	500	505 510
Phe Leu Arg Phe Val Glu Met Met Lys Lys Ile Gly Ile Thr Lys Leu		
	515	520 525
Ser Glu Met Glu Lys Leu Lys Asp Thr Ile Asp Tyr Thr Ala Leu Lys		
	530	535 540
Pro Phe His Cys Thr Ile Leu Val Gln Asn Lys Lys Gly Leu Lys Asn		
545	550	555 560
Leu Tyr Lys Leu Val Ser Asp Ser Tyr Ile Lys Tyr Phe Tyr Gly Val		
	565	570 575
Pro Arg Ile Leu Lys Ser Glu Leu Ile Glu Asn Arg Glu Gly Leu Leu		
	580	585 590
Val Gly Ser Ala Cys Ile Ser Gly Glu Leu Gly Arg Ala Ala Leu Glu		
	595	600 605
Gly Ala Ser Asp Ser Glu Leu Glu Glu Ile Ala Lys Phe Tyr Asp Tyr		

610	615	620
Ile Glu Val Met Pro Leu Asp Val Ile Ala Glu Asp Glu Glu Asp Leu		
625	630	635 640
Asp Arg Glu Arg Leu Lys Glu Val Tyr Arg Lys Leu Tyr Arg Ile Ala		
645	650	655
Lys Lys Leu Asn Lys Phe Val Val Met Thr Gly Asp Val His Phe Leu		
660	665	670
Asp Pro Glu Asp Ala Arg Gly Arg Ala Ala Leu Leu Ala Pro Gln Gly		
675	680	685
Asn Arg Asn Phe Glu Asn Gln Pro Ala Leu Tyr Leu Arg Thr Thr Glu		
690	695	700
Glu Met Leu Glu Lys Ala Ile Glu Ile Phe Glu Asp Glu Glu Ile Ala		
705	710	715 720
Arg Glu Val Val Ile Glu Asn Pro Asn Arg Ile Ala Asp Met Ile Glu		
725	730	735
Glu Val Gln Pro Leu Glu Lys Lys Leu His Pro Pro Ile Ile Glu Asn		
740	745	750
Ala Asp Glu Ile Val Arg Asn Leu Thr Met Lys Arg Ala Tyr Glu Ile		
755	760	765
Tyr Gly Asp Pro Leu Pro Glu Ile Val Gln Lys Arg Val Glu Lys Glu		
770	775	780
Leu Asn Ala Ile Ile Asn His Gly Tyr Ala Val Leu Tyr Leu Ile Ala		
785	790	795 800
Gln Glu Leu Val Gln Lys Ser Met Ser Asp Gly Tyr Val Val Gly Ser		
805	810	815
Arg Gly Ser Val Gly Ser Ser Leu Val Ala Asn Leu Leu Gly Ile Thr		
820	825	830
Glu Val Asn Pro Leu Pro Pro His Tyr Arg Cys Pro Glu Cys Lys Tyr		
835	840	845
Phe Glu Val Val Glu Asp Asp Arg Tyr Gly Ala Gly Tyr Asp Leu Pro		
850	855	860
Asn Lys Asn Cys Pro Arg Cys Gly Ala Pro Leu Arg Lys Asp Gly His		

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Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro						
	885			890		895
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	900			905		910
Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr						
	915			920		925
Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr						
	930			935		940
Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu						
	945			950		955
Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly						
	965			970		975
Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro						
	980			985		990
Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His						
	995			1000		1005
Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu						
	1010			1015		1020
Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly						
	1025			1030		1035
Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile						
	1045			1050		1055
Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser						
	1060			1065		1070
Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg						
	1075			1080		1085
Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg						
	1090			1095		1100
Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg						
	1105			1110		1115
Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys						

1125	1130	1135
Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser		
1140	1145	1150
Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr		
1155	1160	1165
Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe		
1170	1175	1180
Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala		
1185	1190	1195
		1200
Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His		
1205	1210	1215
Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln		
1220	1225	1230
Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg		
1235	1240	1245
Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn		
1250	1255	1260
Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe		
1265	1270	1275
		1280
Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu		
1285	1290	1295
Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu		
1300	1305	1310
Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro		
1315	1320	1325
Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn		
1330	1335	1340
His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu		
1345	1350	1355
		1360
Thr Glu Gln Phe Thr Leu Phe		
1365		

<210> 139  
 <211> 567  
 <212> DNA  
 <213> *Thermatoga maritima*

<400> 139  
 gtgctcgcca tgatatggaa cgacaccgtt ttttgcgtcg tagacacaga aaccacggga 60  
 accgatccct ttgccggaga cgggatatgt gaaatagccg ctgttcctgt cttcaagggg 120  
 aagatctaca gaaacaaagc gtttcaactct ctctgaatc ccagaataag aatccctgcg 180  
 ctgattcaga aagttcacgg tatcagcaac atggacatcg tggaagcgcc agacatggac 240  
 acagtttacg atcttttcag ggattacgtg aagggaacgg tgctcgtgtt tcacaacgcc 300  
 aacttcgacc tcacttttct ggatatgatg gcaaaggaaa cgggaaactt tccaataacg 360  
 aatccctaca tcgacacact cgatctttca gaagagatct ttggaaggcc tcattctctc 420  
 aaatggctct ccgaaagact tggaataaaa accacgatac ggcaccgtgc tttccagat 480  
 gccctgggtga ccgcaagagt ttttgtgaag cttgttgaat ttcttgggtga aaacaggggc 540  
 aacgaattca tacgtggaaa acggggg 567

<210> 140  
 <211> 189  
 <212> PRT  
 <213> *Thermatoga maritima*

<400> 140  
 Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr  
 1 5 10 15  
 Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile  
 20 25 30  
 Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe  
 35 40 45  
 His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys  
 50 55 60  
 Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp  
 65 70 75 80  
 Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val  
 85 90 95  
 Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys  
 100 105 110  
 Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp  
 115 120 125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser  
 130 135 140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp  
 145 150 155 160

Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly  
 165 170 175

Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly  
 180 185

<210> 141  
 <211> 1434  
 <212> DNA  
 <213> *Thermatoga maritima*

<400> 141  
 gtggaagttc ttacaggaa gtacaggcca aagacttttt ctgaggttgt caatcaggat 60  
 catgtgaaga aggcaataat cgtgtctatt cagaagaaca gcgtggccca cggatacata 120  
 ttcgccggtc cgaggggaac ggggaagact actcttgcca gaattctcgc aaaatccctg 180  
 aactgtgaga acagaaaagg agttgaaccc tgcaattcct gcagagcctg cagagagata 240  
 gacgaggga ccttcatgga cgtgatagag ctgcacgcgg cctccaacag aggaatagac 300  
 gagatcagaa gaatcagaga cgccgttgga tacaggccga tggaaggtaa atacaaagtc 360  
 tacataatag acgaagttca catgctcacg aaagaagcct tcaacgcgct cctcaaaaca 420  
 ctogaagaac ctccctccca cgtcgtgttc gtgctggcaa cgacaaacct tgagaagggt 480  
 cctccacaga ttatctcgag atgtcagggt ttcgagttca gaaacattcc cgacgagctc 540  
 atcgaagaaga ggctccagga agttgcggag gctgaaggaa tagagataga cagggaagct 600  
 ctgagcttca tcgcaaaaag agcctctgga ggcttgagag acgcgctcac catgctcgag 660  
 caggtgtgga agttctcgga aggaaagata gatctcgaga cggtagacag ggcgctcggg 720  
 ttgataccga tacagggtgt tcgcgattac gtgaacgcta tcttttctgg tgatgtgaaa 780  
 aggggtcttca cgttctcgga cgacgtctat tacagcggga aggactacga ggtgctcatt 840  
 caggaagcag tcgaggatct ggtcgaagac ctggaaaggg agagaggggt ttaccagggt 900  
 tcagcgaacg atatagttca ggttctcgaga caacttctga atcttctgag agagataaag 960  
 ttcgccgaag aaaaacgact cgtctgtaaa gtgggttcgg cttacatagc gacgaggttc 1020  
 tccaccacaa acgttcagga aaacgatgtc agagaaaaaa acgataattc aaatgtacag 1080  
 cagaaagaag agaagaaaga aacggtgaag gcaaaagaag aaaaacagga agacagcgag 1140  
 ttcgagaaac gcttcaaaga actcatggaa gaactgaaag aaaagggcga tctctctatc 1200  
 tttgtcgctc tcagcctctc agaggtgcag tttgacggag aaaaggtgat tatttctttt 1260  
 gattcatcga aagctatgca ttacgagttg atgaagaaaa aactgcctga gctggaaaac 1320  
 attttttcta gaaaactcgg gaaaaaagta gaagttgaac ttcgactgat gggaaaagaa 1380  
 gaaacaatcg agaaggtttc tcagaagatc ctgagattgt ttgaacagga ggga 1434

<210> 142  
 <211> 478  
 <212> PRT

<213> *Thermatoga maritima*

<400> 142

Met	Glu	Val	Leu	Tyr	Arg	Lys	Tyr	Arg	Pro	Lys	Thr	Phe	Ser	Glu	Val
1				5					10					15	
Val	Asn	Gln	Asp	His	Val	Lys	Lys	Ala	Ile	Ile	Gly	Ala	Ile	Gln	Lys
			20					25					30		
Asn	Ser	Val	Ala	His	Gly	Tyr	Ile	Phe	Ala	Gly	Pro	Arg	Gly	Thr	Gly
		35					40					45			
Lys	Thr	Thr	Leu	Ala	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Asn	Cys	Glu	Asn
	50					55					60				
Arg	Lys	Gly	Val	Glu	Pro	Cys	Asn	Ser	Cys	Arg	Ala	Cys	Arg	Glu	Ile
65					70					75					80
Asp	Glu	Gly	Thr	Phe	Met	Asp	Val	Ile	Glu	Leu	Asp	Ala	Ala	Ser	Asn
				85					90						95
Arg	Gly	Ile	Asp	Glu	Ile	Arg	Arg	Ile	Arg	Asp	Ala	Val	Gly	Tyr	Arg
		100						105					110		
Pro	Met	Glu	Gly	Lys	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	His	Met
		115					120					125			
Leu	Thr	Lys	Glu	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro
	130					135					140				
Pro	Ser	His	Val	Val	Phe	Val	Leu	Ala	Thr	Thr	Asn	Leu	Glu	Lys	Val
145					150					155					160
Pro	Pro	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Val	Phe	Glu	Phe	Arg	Asn	Ile
			165					170						175	
Pro	Asp	Glu	Leu	Ile	Glu	Lys	Arg	Leu	Gln	Glu	Val	Ala	Glu	Ala	Glu
		180						185					190		
Gly	Ile	Glu	Ile	Asp	Arg	Glu	Ala	Leu	Ser	Phe	Ile	Ala	Lys	Arg	Ala
	195						200					205			
Ser	Gly	Gly	Leu	Arg	Asp	Ala	Leu	Thr	Met	Leu	Glu	Gln	Val	Trp	Lys
	210					215					220				
Phe	Ser	Glu	Gly	Lys	Ile	Asp	Leu	Glu	Thr	Val	His	Arg	Ala	Leu	Gly
225					230					235					240

Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser  
                   245                  250                  255  
 Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser  
                   260                  265                  270  
 Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val  
                   275                  280                  285  
 Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp  
                   290                  295                  300  
 Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys  
 305                  310                  315                  320  
 Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile  
                   325                  330                  335  
 Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu  
                   340                  345                  350  
 Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr  
                   355                  360                  365  
 Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg  
                   370                  375                  380  
 Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile  
 385                  390                  395                  400  
 Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val  
                   405                  410                  415  
 Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys  
                   420                  425                  430  
 Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys  
                   435                  440                  445  
 Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu  
                   450                  455                  460  
 Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly  
 465                  470                  475

<210> 143  
 <211> 1098



<212> DNA

<213> *Thermatoga maritima*

<400> 143

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atgaaagtaa ccgtcacgac tcttgaattg aaagacaaaa taaccatcgc ctcaaaagcg 60
ctcgcaaaga aatccgtgaa acccattctt gctggatttc ttttcgaagt gaaagatgga 120
aatttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacg ttttgtggta ccaggagatg tcattcagaa gatggtcaag 240
gttctcccag atgagataac ggaactttct ttagaggggg atgctcttgt tataagttct 300
ggaagcaccg ttttcaggat caccaccatg cccgcggacg aatttccaga gataacgcct 360
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat gggtgaaaag 420
gtcatcttcg ccgctgccaa agacgagttc atgcgaaatc tgaatggagt tttctgggaa 480
ctccacaaga atcttctcag gctggttgca agtgatgggt tcagacttgc acttgctgaa 540
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600
gttcaaaacg tgctggacaa cacaacggag ccgactataa cggtgaggta cgatggaaga 660
agggtttctc tgtcgacaaa tgatgtagaa acggtgatga gagtggtcga cgctgaattt 720
cccgattaca aaaggggtgat ccccgaaact ttcaaaacga aagtggtggt ttccagaaaa 780
gaactcaggg aatctttgaa gaggggtgat gtgattgcca gcaaggggaag cgagtccgtg 840
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagcccgga ttatggagaa 900
gtggtcgatg aagttgaagt tcaaaaagaa ggggaagatc tcgtgatcgc tttcaaccgc 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggatacct ttacatagtg 1080
atgcccatca gactggca                                     1098
```

<210> 144

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

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Met Lys Val Thr Val Thr Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile
  1                      5                      10                      15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly
      20                      25                      30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp
      35                      40                      45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly
      50                      55                      60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys
      65                      70                      75                      80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu
      85                      90                      95
```

Val Ile Ser Ser Gly Ser Thr Val Phe Arg Ile Thr Thr Met Pro Ala  
100 105 110  
Asp Glu Phe Pro Glu Ile Thr Pro Ala Glu Ser Gly Ile Thr Phe Glu  
115 120 125  
Val Asp Thr Ser Leu Leu Glu Glu Met Val Glu Lys Val Ile Phe Ala  
130 135 140  
Ala Ala Lys Asp Glu Phe Met Arg Asn Leu Asn Gly Val Phe Trp Glu  
145 150 155 160  
Leu His Lys Asn Leu Leu Arg Leu Val Ala Ser Asp Gly Phe Arg Leu  
165 170 175  
Ala Leu Ala Glu Glu Gln Ile Glu Asn Glu Glu Glu Ala Ser Phe Leu  
180 185 190  
Leu Ser Leu Lys Ser Met Lys Glu Val Gln Asn Val Leu Asp Asn Thr  
195 200 205  
Thr Glu Pro Thr Ile Thr Val Arg Tyr Asp Gly Arg Arg Val Ser Leu  
210 215 220  
Ser Thr Asn Asp Val Glu Thr Val Met Arg Val Val Asp Ala Glu Phe  
225 230 235 240  
Pro Asp Tyr Lys Arg Val Ile Pro Glu Thr Phe Lys Thr Lys Val Val  
245 250 255  
Val Ser Arg Lys Glu Leu Arg Glu Ser Leu Lys Arg Val Met Val Ile  
260 265 270  
Ala Ser Lys Gly Ser Glu Ser Val Lys Phe Glu Ile Glu Glu Asn Val  
275 280 285  
Met Arg Leu Val Ser Lys Ser Pro Asp Tyr Gly Glu Val Val Asp Glu  
290 295 300  
Val Glu Val Gln Lys Glu Gly Glu Asp Leu Val Ile Ala Phe Asn Pro  
305 310 315 320  
Lys Phe Ile Glu Asp Val Leu Lys His Ile Glu Thr Glu Glu Ile Glu  
325 330 335  
Met Asn Phe Val Asp Ser Thr Ser Pro Cys Gln Ile Asn Pro Leu Asp  
340 345 350

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala  
 355 360 365

<210> 145  
 <211> 972  
 <212> DNA  
 <213> *Thermatoga maritima*

<400> 145  
 atgccagtca cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60  
 ctccctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120  
 gatttcataa ggtctttact caggacaaag acgatctttt ccaacaagac gatcattgac 180  
 atcgtcaatt tcgatgagtg gaaagcacag gagcagaagc gtctcgttga acttttgaaa 240  
 aacgtaccgg aagacgttca tatcttcacg cgttctcaaa aaacaggtgg aaagggagta 300  
 gcgctggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtggat agaaaagcgc 360  
 ttcagggaga atggtttgct catcgataaa gatgcccttc agctgttttt ctccaagggt 420  
 ggaacgaacg acctgatcat agaaaggag attgaaaaac tgaaagctta ttccgaggac 480  
 agaaagataa cggtagaaga cgtggaagag gtcgttttta cctatcagac tccgggatac 540  
 gatgattttt gctttgctgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600  
 cagctgtgga aaaccacaga gtccgtggtg attgccactg tccttgcgaa tcacttcttg 660  
 gatctcttca aaatcctcgt tcttgtagaca aagaaaagat actacacctg gcctgatgtg 720  
 tccaggggtg ccaaagagct gggaattccc gttcctcgtg tggctcgttt cctcggtttc 780  
 tcctttaaga cctggaaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840  
 gtagaaaaga tactgagggg tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900  
 ccaaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960  
 agagatgaag aa 972

<210> 146  
 <211> 324  
 <212> PRT  
 <213> *Thermatoga maritima*

<400> 146  
 Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu  
 1 5 10 15  
 Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile  
 20 25 30  
 His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg  
 35 40 45  
 Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe  
 50 55 60

Asp	Glu	Trp	Lys	Ala	Gln	Glu	Gln	Lys	Arg	Leu	Val	Glu	Leu	Leu	Lys	65	70	75	80
Asn	Val	Pro	Glu	Asp	Val	His	Ile	Phe	Ile	Arg	Ser	Gln	Lys	Thr	Gly	85	90	95	
Gly	Lys	Gly	Val	Ala	Leu	Glu	Leu	Pro	Lys	Pro	Trp	Glu	Thr	Asp	Lys	100	105	110	
Trp	Leu	Glu	Trp	Ile	Glu	Lys	Arg	Phe	Arg	Glu	Asn	Gly	Leu	Leu	Ile	115	120	125	
Asp	Lys	Asp	Ala	Leu	Gln	Leu	Phe	Phe	Ser	Lys	Val	Gly	Thr	Asn	Asp	130	135	140	
Leu	Ile	Ile	Glu	Arg	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Tyr	Ser	Glu	Asp	145	150	155	160
Arg	Lys	Ile	Thr	Val	Glu	Asp	Val	Glu	Glu	Val	Val	Phe	Thr	Tyr	Gln	165	170	175	
Thr	Pro	Gly	Tyr	Asp	Asp	Phe	Cys	Phe	Ala	Val	Ser	Glu	Gly	Lys	Arg	180	185	190	
Lys	Leu	Ala	His	Ser	Leu	Leu	Ser	Gln	Leu	Trp	Lys	Thr	Thr	Glu	Ser	195	200	205	
Val	Val	Ile	Ala	Thr	Val	Leu	Ala	Asn	His	Phe	Leu	Asp	Leu	Phe	Lys	210	215	220	
Ile	Leu	Val	Leu	Val	Thr	Lys	Lys	Arg	Tyr	Tyr	Thr	Trp	Pro	Asp	Val	225	230	235	240
Ser	Arg	Val	Ser	Lys	Glu	Leu	Gly	Ile	Pro	Val	Pro	Arg	Val	Ala	Arg	245	250	255	
Phe	Leu	Gly	Phe	Ser	Phe	Lys	Thr	Trp	Lys	Phe	Lys	Val	Met	Asn	His	260	265	270	
Leu	Leu	Tyr	Tyr	Asp	Val	Lys	Lys	Val	Arg	Lys	Ile	Leu	Arg	Asp	Leu	275	280	285	
Tyr	Asp	Leu	Asp	Arg	Ala	Val	Lys	Ser	Glu	Glu	Asp	Pro	Lys	Pro	Phe	290	295	300	
Phe	His	Glu	Phe	Ile	Glu	Glu	Val	Ala	Leu	Asp	Val	Tyr	Ser	Leu	Gln	305	310	315	320

Arg Asp Glu Glu

<210> 147

<211> 936

<212> DNA

<213> *Thermatoga maritima*

<400> 147

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atgaacgatt tgatcagaaa gtacgctaaa gatcaactgg aaactttgaa aaggatcata 60
gaaaagtctg aaggaatata catcctcata aatggagaag atctctcgta tccgagagaa 120
gtatcccttg aacttcccgga gtacgtggag aaatttcccc cgaaggcctc ggatgtttctg 180
gagatagatc ccgaggggga gaacatagga atagacgaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300
atgaccagc aggcggcgaa cgcgtttctg aaggcccttg aagaaccacc agaatacgct 360
gtgatcggtc tgaacactcg ccgctggcat tatctactgc cgacgataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaagcctac 540
aaacttggtg cggaaaaact ttctggattg atggaaagtc tcaaagtgtt ggagacggaa 600
aaactcttga aaaaggtcct ttcaaaaggc ctcaagggtt atctcgcatg tagggagctc 660
ctggagagat tttcaaagggt ggaatcgaag gaattctttg cgctttttga tcaggtgact 720
aacacgataa caggaaaaga cgcgtttctt ttgatccaga gactgacaag aatcattctc 780
cacgaaaaca catgggaaaag cggtgaagat caaaaaagcg tgtctttcct cgattcaatt 840
ctcaggggtga agatagcgaa tctgaacaac aaactcactc tgatgaacat cctcgcgata 900
cacagagaga gaaagagagg tgtcaacgct tggagc 936
```

<210> 148

<211> 311

<212> PRT

<213> *Thermatoga maritima*

<400> 148

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Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
  1             5             10            15

Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
      20             25            30

Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
      35             40            45

Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
      50             55            60

Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
      65             70            75            80
```

Leu	Asn	Tyr	Ser	Pro	Glu	Leu	Tyr	Thr	Arg	Lys	Tyr	Val	Ile	Val	His	
				85					90					95		
Asp	Cys	Glu	Arg	Met	Thr	Gln	Gln	Ala	Ala	Asn	Ala	Phe	Leu	Lys	Ala	
			100					105					110			
Leu	Glu	Glu	Pro	Pro	Glu	Tyr	Ala	Val	Ile	Val	Leu	Asn	Thr	Arg	Arg	
		115					120					125				
Trp	His	Tyr	Leu	Leu	Pro	Thr	Ile	Lys	Ser	Arg	Val	Phe	Arg	Val	Val	
	130					135					140					
Val	Asn	Val	Pro	Lys	Glu	Phe	Arg	Asp	Leu	Val	Lys	Glu	Lys	Ile	Gly	
145					150					155					160	
Asp	Leu	Trp	Glu	Glu	Leu	Pro	Leu	Leu	Glu	Arg	Asp	Phe	Lys	Thr	Ala	
			165					170						175		
Leu	Glu	Ala	Tyr	Lys	Leu	Gly	Ala	Glu	Lys	Leu	Ser	Gly	Leu	Met	Glu	
		180						185					190			
Ser	Leu	Lys	Val	Leu	Glu	Thr	Glu	Lys	Leu	Leu	Lys	Lys	Val	Leu	Ser	
	195						200					205				
Lys	Gly	Leu	Glu	Gly	Tyr	Leu	Ala	Cys	Arg	Glu	Leu	Leu	Glu	Arg	Phe	
	210					215					220					
Ser	Lys	Val	Glu	Ser	Lys	Glu	Phe	Phe	Ala	Leu	Phe	Asp	Gln	Val	Thr	
225					230					235					240	
Asn	Thr	Ile	Thr	Gly	Lys	Asp	Ala	Phe	Leu	Leu	Ile	Gln	Arg	Leu	Thr	
			245						250					255		
Arg	Ile	Ile	Leu	His	Glu	Asn	Thr	Trp	Glu	Ser	Val	Glu	Asp	Lys	Ser	
		260						265					270			
Val	Ser	Phe	Leu	Asp	Ser	Ile	Leu	Arg	Val	Lys	Ile	Ala	Asn	Leu	Asn	
		275					280					285				
Asn	Lys	Leu	Thr	Leu	Met	Asn	Ile	Leu	Ala	Ile	His	Arg	Glu	Arg	Lys	
	290					295					300					
Arg	Gly	Val	Asn	Ala	Trp	Ser										
305					310											

<210> 149

<211> 423  
 <212> DNA  
 <213> *Thermatoga maritima*

<400> 149  
 atgtctttct tcaacaagat cataactcata ggaagactcg tgagagatcc cgaagagaga 60  
 tacacgctca gcggaactcc agtcaccacc ttcaccatag cggtaggacag gggtcccaga 120  
 aagaacgcgc cggacgacgc tcaaacgact gatttcttca ggatcgtcac ctttggaaga 180  
 ctggcagagt tcgctagaac ctatctcacc aaaggaaggc tcgttctcgt cgaagggtgaa 240  
 atgagaatga gaagatggga aacacccact ggagaaaaga gggatatctcc ggaggttgtc 300  
 gcaaacggtt ttagattcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360  
 gagctggaaa taccggaaga agacttttcc agcgatacct tcagtgaaga tgaaccacca 420  
 ttt 423

<210> 150  
 <211> 141  
 <212> PRT  
 <213> *Thermatoga maritima*

<400> 150  
 Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp  
 1 5 10 15  
 Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr  
 20 25 30  
 Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln  
 35 40 45  
 Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe  
 50 55 60  
 Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu  
 65 70 75 80  
 Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser  
 85 90 95  
 Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala  
 100 105 110  
 Glu Thr Val Ser Glu Thr Glu Glu Glu Leu Glu Ile Pro Glu Glu Asp  
 115 120 125  
 Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe  
 130 135 140

<210> 151  
 <211> 1353  
 <212> DNA  
 <213> *Thermatoga maritima*

<400> 151  
 atgctgtgttc ccccgacacaa cttagaggcc gaagttgctg tgctcggaag catattgata 60  
 gatccgtcgg taataaacga cgttcttgaa attttgagcc acgaagattt ctatctgaaa 120  
 aaacaccaac acatcttcag agcgatggaa gagctttacg acgaaggaaa accggtggac 180  
 gtgggtttccg tctgtgacaa gcttcaaagc atgggaaaac tcgaggaagt aggtggagat 240  
 ctggaagtgg cccagctcgc tgaggctgtg ccagttctg cacacgcact tcaactacgcg 300  
 gagatcgtca aggaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360  
 gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgata 420  
 ttcgagatct cagagatgaa aacgacaaaa tcctacgata atctgagagg catcatgcac 480  
 cgggtgtttg aaaacctgga gaacttcagg gaaagagcca accttataga acccggtgtg 540  
 ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac aggggtccac 600  
 agtccgatac tgggtgataat agcagcgaga ccctccatgg gaaaaacctc ctccgcactc 660  
 tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720  
 atgtccaagg aacagctcgc tcaaagacta ctgagcatgg agtccggtgt ggatctttac 780  
 agcatcagaa caggatacct ggatcaggag aagtgggaaa gactcacaat agcggtcttct 840  
 aaactctaca aagcaccatc agttgtggac gatgagtcac tcctcgatcc gcgatcggtg 900  
 agggcaaaaag cgagaaggat gaaaaaagaa tacgatgtaa aagccatttt tgctcgactat 960  
 ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagatc 1020  
 tcgagatctc tgaagctcct tgcgagggaa ctgcacatag tggatgatagc gctttcacag 1080  
 ctttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtga cctcagggaa 1140  
 tccggtgcga tagaacagga cgcagacaca gtcattctca tctacagggg ggaatattac 1200  
 aggagcaaaa aatccaaaga ggaaagcaag cttcacgaac ctcacgaagc tgaaatcata 1260  
 ataggtaaac agagaaacgg tcccgttgga acgatcactc tgatcttcga cccagaacg 1320  
 gttacgttcc atgaagtcga tgtggtgcat tca 1353

<210> 152  
 <211> 451  
 <212> PRT  
 <213> *Thermatoga maritima*

<400> 152  
 Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly  
 1 5 10 15  
 Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu  
 20 25 30  
 Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala  
 35 40 45  
 Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val



50		55		60
Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp				
65		70		75
Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala				
	85		90	95
Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu				
	100		105	110
Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp				
	115		120	125
Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser				
	130		135	140
Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His				
145		150		155
Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile				
	165		170	175
Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu				
	180		185	190
Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala				
	195		200	205
Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg				
	210		215	220
Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu				
225		230		235
Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly				
	245		250	255
Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp				
	260		265	270
Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val				
	275		280	285
Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala				
	290		295	300
Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr				

305                      310                      315                      320  
 Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu  
                                  325                      330                      335  
 Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp  
                                  340                      345                      350  
 Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg  
                                  355                      360                      365  
 Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile  
                                  370                      375                      380  
 Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr  
 385                                   390                      395                      400  
 Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu  
                                  405                      410                      415  
 Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile  
                                  420                      425                      430  
 Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val  
                                  435                      440                      445  
 Val His Ser  
 450

<210> 153  
 <211> 1695  
 <212> DNA  
 <213> *Thermatoga maritima*

<400> 153  
 gtgattcctc gagaggatcat cgaggaaata aaagaaaagg ttgacatcgt agaggtcatt 60  
 tccgagtacg tgaatcttac ccgggtaggt tcctcctaca gggctctctg tccctttcat 120  
 tcagaaacca atccttcttt ctacgttcat ccgggtttga agatatacca ttgtttcggc 180  
 tgcggtgcga gtggagacgt catcaaattt cttcaagaaa tggaagggat cagtttccag 240  
 gaagcgctgg aaagacttgc caaaagagct gggattgatc tttctctcta cagaacagaa 300  
 gggacttctg aatacggaaa atacattcgt ttgtacgaag aaacgtggaa aaggtacgtc 360  
 aaagagctgg agaaatcgaa agaggcaaaa gactatttaa aaagcagagg cttctctgaa 420  
 gaagatatag caaagtctcg ctttgggtac gtccccaaga gatccagcat ctctatagaa 480  
 gttgcagaag gcatgaacat aacactggaa gaacttgtca gatacgggtat cgcgctgaaa 540  
 aagggatgat gattcgttga tagattcgaa ggaagaatcg ttgttccaat aaagaacgac 600  
 agtggtcata ttgtggcttt tgggtggcgt gctctcggca acgaagaacc gaagtatttg 660  
 aactctccag agaccaggta tttttcgaag aagaagaccc tttttctctt cgatgaggcg 720

```

aaaaaagtgg caaaagaggt tggttttttc gtcatcaccg aaggctactt cgacgcgctc 780
gcattcagaa aggatggaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaactttc ggcgatttcg aaaaacgtca tactgtgttt cgataatgac 900
aaagcaggct tcagagccac tctcaaatcc ctcgaggatc tcctagacta cgaattcaac 960
gtgcttgtgg caacccccctc tccttataaaa gaccagatg aactctttca gaaagaagga 1020
gaaggttcat tgaaaaagat gctgaaaaac tcgctgttcg tcgaatatct tctggtgacg 1080
gctggtgagg tcttctttga caggaacagc cccgcgggtg tgagatccta ctttctttc 1140
ctcaaagggt gggccaaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtgaatgagg tttcatcttc tctccagata ccagaaaacc agattttgaa cttttttgaa 1260
agcgacaggt ctaacactat gcctgttcat gagaccaagt cgtcaaagggt ttacgatgag 1320
gggagaggac tggcttattt gtttttgaac tacgaggatt tgagggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaaac gcgagggagt ttttcaagag agtctcactg 1440
ggagaagatt tgaacaaagt catagaaaac ttcccaaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tcctccaaag gatcccgaga aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgcag aaatagatga tatgataaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtgga tctcctcaga 1680
aaaataaaga ggagg                                     1695

```

<210> 154

<211> 565

<212> PRT

<213> *Thermatoga maritima*

<400> 154

```

Met Ile Pro Arg Glu Val Ile Glu Glu Ile Lys Glu Lys Val Asp Ile
  1               5               10               15

```

```

Val Glu Val Ile Ser Glu Tyr Val Asn Leu Thr Arg Val Gly Ser Ser
      20               25               30

```

```

Tyr Arg Ala Leu Cys Pro Phe His Ser Glu Thr Asn Pro Ser Phe Tyr
      35               40               45

```

```

Val His Pro Gly Leu Lys Ile Tyr His Cys Phe Gly Cys Gly Ala Ser
      50               55               60

```

```

Gly Asp Val Ile Lys Phe Leu Gln Glu Met Glu Gly Ile Ser Phe Gln
      65               70               75               80

```

```

Glu Ala Leu Glu Arg Leu Ala Lys Arg Ala Gly Ile Asp Leu Ser Leu
      85               90               95

```

```

Tyr Arg Thr Glu Gly Thr Ser Glu Tyr Gly Lys Tyr Ile Arg Leu Tyr
      100              105              110

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```

Glu Glu Thr Trp Lys Arg Tyr Val Lys Glu Leu Glu Lys Ser Lys Glu
      115              120              125

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Ala Lys Asp Tyr Leu Lys Ser Arg Gly Phe Ser Glu Glu Asp Ile Ala  
 130 135 140  
 Lys Phe Gly Phe Gly Tyr Val Pro Lys Arg Ser Ser Ile Ser Ile Glu  
 145 150 155 160  
 Val Ala Glu Gly Met Asn Ile Thr Leu Glu Glu Leu Val Arg Tyr Gly  
 165 170 175  
 Ile Ala Leu Lys Lys Gly Asp Arg Phe Val Asp Arg Phe Glu Gly Arg  
 180 185 190  
 Ile Val Val Pro Ile Lys Asn Asp Ser Gly His Ile Val Ala Phe Gly  
 195 200 205  
 Gly Arg Ala Leu Gly Asn Glu Glu Pro Lys Tyr Leu Asn Ser Pro Glu  
 210 215 220  
 Thr Arg Tyr Phe Ser Lys Lys Lys Thr Leu Phe Leu Phe Asp Glu Ala  
 225 230 235 240  
 Lys Lys Val Ala Lys Glu Val Gly Phe Phe Val Ile Thr Glu Gly Tyr  
 245 250 255  
 Phe Asp Ala Leu Ala Phe Arg Lys Asp Gly Ile Pro Thr Ala Val Ala  
 260 265 270  
 Val Leu Gly Ala Ser Leu Ser Arg Glu Ala Ile Leu Lys Leu Ser Ala  
 275 280 285  
 Tyr Ser Lys Asn Val Ile Leu Cys Phe Asp Asn Asp Lys Ala Gly Phe  
 290 295 300  
 Arg Ala Thr Leu Lys Ser Leu Glu Asp Leu Leu Asp Tyr Glu Phe Asn  
 305 310 315 320  
 Val Leu Val Ala Thr Pro Ser Pro Tyr Lys Asp Pro Asp Glu Leu Phe  
 325 330 335  
 Gln Lys Glu Gly Glu Gly Ser Leu Lys Lys Met Leu Lys Asn Ser Arg  
 340 345 350  
 Ser Phe Glu Tyr Phe Leu Val Thr Ala Gly Glu Val Phe Phe Asp Arg  
 355 360 365  
 Asn Ser Pro Ala Gly Val Arg Ser Tyr Leu Ser Phe Leu Lys Gly Trp  
 370 375 380

Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu  
385 390 395 400

Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu  
405 410 415

Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr  
420 425 430

Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe  
435 440 445

Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu  
450 455 460

Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu  
465 470 475 480

Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys  
485 490 495

Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro  
500 505 510

Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile  
515 520 525

Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn  
530 535 540

Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg  
545 550 555 560

Lys Ile Lys Arg Arg  
565

<210> 155

<211> 804

<212> DNA

<213> *Thermus thermophilus*

<400> 155

atggctctac acccggtctca ccctgggggca ataatcgggc acgaggccgt tctcgccctc 60  
cttccccgcc tcaccgccca gacctgctc ttctccggcc ccgagggggg gggcgggcgc 120  
accgtggccc gctggtacgc ctgggggctc aaccgcggct tccccccgcc ctccctgggg 180  
gagcaccgac acgtcctcga ggtggggccc aaggcccgga acctccggg ccgggccgag 240

gtgcggtggtg aggaggtggc gcccctcttg gagtgggtgct ccagccaccc ccgggagcgg 300  
 gtgaaggtgg ccatacctgga ctcggtccac ctctcaccg aggcgcgcgc caacgccctc 360  
 ctcaagctcc tggaggagcc cccttcctac gcccgcatcg tctcatcgcc cccaagccgc 420  
 gccaccctcc tccccaccct ggcctcccg ggcacggagg tggcattcgc ccccggtgcc 480  
 gaggaggccc tgcgcgccct caccacaggac ccggagctcc tccgctacgc cgccggggcc 540  
 ccgggcccgc tccttagggc cctccaggac ccggaggggt accggggccg catggccagg 600  
 gcgcaaaggg tcctgaaagc cccgcccctg gagcgctcg ctttgcttcg ggagcttttg 660  
 gccgaggagg aggggggtcca cgccctccac gccgtcctaa agcgcccgga gcacctcctt 720  
 gccctggagc gggcgcgga ggcctggag ggtacgtga gccccgagct ggtcctcgcc 780  
 cggctggcct tagacttaga gaca 804

<210> 156  
 <211> 268  
 <212> PRT  
 <213> *Thermus thermophilus*

<400> 156  
 Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala  
 1 5 10 15  
 Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser  
 20 25 30  
 Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp  
 35 40 45  
 Gly Leu Asn Arg Gly Phe Pro Pro Pro Ser Leu Gly Glu His Pro Asp  
 50 55 60  
 Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu  
 65 70 75 80  
 Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His  
 85 90 95  
 Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu  
 100 105 110  
 Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro  
 115 120 125  
 Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu  
 130 135 140  
 Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro  
 145 150 155 160

Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr  
                   165                  170                  175  
 Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu  
                   180                  185                  190  
 Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro  
                   195                  200                  205  
 Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu  
                   210                  215                  220  
 Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu  
 225                  230                  235                  240  
 Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu  
                   245                  250                  255  
 Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr  
                   260                  265

<210> 157  
 <211> 729  
 <212> DNA  
 <213> *Thermus thermophilus*

<400> 157  
 atgctggacc tgagggaggt gggggaggcg gagtggaagg ccctaaagcc ccttttggaa 60  
 agcgtgcccc agggcgcccc cgctctcctc ctggacccta agccaagccc ctcccgggcg 120  
 gccttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctggtg 180  
 cggcacctgg aaaaccgggc caagcgcttg gggctcaggc tcccgggcgg ggtggcccag 240  
 tacctggcct ccctggaggg ggacctcgag gcctggagc gggagctgga gaagcttgcc 300  
 ctctctctcc caccctcac cctggagaag gtggagaagg tggaggccct gaggcccccc 360  
 ctacggggt ttgacctggt gcgctccgtc ctggagaagg accccaagga ggccctcctg 420  
 cgcctaggcg gcctcaagga ggagggggag gagccctca ggctcctcgg ggccctctcc 480  
 tggcagttcg cctcctcgc ccgggccttc ttctcctcc gggaaaacc caggcccaag 540  
 gaggaggacc tcgcccgcct cgaggccac ccctacgccg ccgcccgcgc cctggaggcg 600  
 gcgaagcgcc tcacggaaga ggccctcaag gaggccttg acgccctcat ggaggcggaa 660  
 aagagggcca agggggggaa agaccctgg ctgccttg aggcggcggt cctccgcctc 720  
 gcccgttga 729

<210> 158  
 <211> 292  
 <212> PRT  
 <213> *Thermus thermophilus*

<400> 158

Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu  
1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr  
20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly  
35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala  
50 55 60

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu  
65 70 75 80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg  
85 90 95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His  
100 105 110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val  
115 120 125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg  
130 135 140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys  
145 150 155 160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu  
165 170 175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu  
180 185 190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala  
195 200 205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg  
210 215 220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His  
225 230 235 240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu  
245 250 255



Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg  
260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu  
275 280 285

Arg Leu Ala Arg  
290

<210> 159  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 159  
gtgtgtcata tgagtaagga tttcgtccac cttcacc 37

<210> 160  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 160  
gtgtgtggat ccgggggacta ctcggaagta aggg 34

<210> 161  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 161  
gtgtgtcata tggaaccac aatattccag ttccag 36

<210> 162

<211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 162  
 gtgtgtggat ccttatccac catgagaagt atttttcac 39  
  
  
 <210> 163  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 163  
 gtgtgtcata tggaaaaagt tttttttgga aaaaactcca g 41  
  
  
 <210> 164  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 164  
 gtgtgtggat ccttaatccg cctgaacggc taacg 35  
  
  
 <210> 165  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 165  
 gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g 41  
  
  
 <210> 166

<211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 166  
 gtgtgtggat ccttaaaaca gcctcgcccc gctgga 36  
  
 <210> 167  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 167  
 gtgtgtcata tgcgcgttaa ggtggacagg gag 33  
  
 <210> 168  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 168  
 tgtgtctcga gtcattggcta caccctcatc ggcatt 35  
  
 <210> 169  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 169  
 gtgtgtcata tgctcaataa ggtttttata ataggaagac ttacggg 47  
  
 <210> 170

<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 170

gtgtggatcc ttaaaaaggt atttcgtcct cttcatcgg

39

<210> 171

<211> 807

<212> DNA

<213> Thermus thermophilus

<400> 171

atggctcgag gcctgaaccg cgttttcttc atcggcgccc tcgccacccg gccggacatg 60  
cgctacacccc cggcgggggt cgccattttg gacctgacct tcgccgggtca ggacctgctt 120  
ctttccgata acggggggga accggaggtg tcctgggtacc accgggtgag gctcttaggc 180  
cgccaggcgg agatgtgggg cgacctcttg gaccaagggc agctcgtctt cgtggagggc 240  
cgcttgaggt accgccagtg ggaaagggag ggggagaagc ggagcgagct ccagatccgg 300  
gccgacttcc ggacccccctg gacgaccggg ggaagaagcg ggcgaggagc agccggggcc 360  
agcccagggt ccgcgcgcc ctgaaccagg tcttcctcat gggcaacctg acccgggacc 420  
cggaactccg ctacaccccc cagggcaccg cggtgggccc gctgggcctg gcggtgaacg 480  
agcgccgcca gggggcgagg gagcgacccc acttcgtgga ggttcaggcc tggcgcgacc 540  
tggcgaggatg ggccgcccag ctgaggaagg gcgacggcct tttcgtgatc ggcaggttgg 600  
tgaacgactc ctggaccagc tccagcggcg agcggcgctt ccagaccgt gtggaggccc 660  
tcaggctgga gcgccccacc cgtggacctg cccaggcctg cccaggccgg cggaacaggt 720  
cccgcgaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac tttccgcccg 780  
aggaggattt gccgttttga gcacgaa 807

<210> 172

<211> 266

<212> PRT

<213> Thermus thermophilus

<400> 172

Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr  
1 5 10 15

Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu  
20 25 30

Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro  
35 40 45

Glu Val Ser Trp Tyr His Arg Val Arg Leu Leu Gly Arg Gln Ala Glu  
 50 55 60  
 Met Trp Gly Asp Leu Leu Asp Gln Gly Gln Leu Val Phe Val Glu Gly  
 65 70 75 80  
 Arg Leu Glu Tyr Arg Gln Trp Glu Arg Glu Gly Glu Lys Arg Ser Glu  
 85 90 95  
 Leu Gln Ile Arg Ala Asp Phe Leu Asp Pro Leu Asp Asp Arg Gly Lys  
 100 105 110  
 Lys Arg Ala Glu Asp Ser Arg Gly Gln Pro Arg Leu Arg Ala Ala Leu  
 115 120 125  
 Asn Gln Val Phe Leu Met Gly Asn Leu Thr Arg Asp Pro Glu Leu Arg  
 130 135 140  
 Tyr Thr Pro Gln Gly Thr Ala Val Ala Arg Leu Gly Leu Ala Val Asn  
 145 150 155 160  
 Glu Arg Arg Gln Gly Ala Glu Glu Arg Thr His Phe Val Glu Val Gln  
 165 170 175  
 Ala Trp Arg Asp Leu Ala Glu Trp Ala Ala Glu Leu Arg Lys Gly Asp  
 180 185 190  
 Gly Leu Phe Val Ile Gly Arg Leu Val Asn Asp Ser Trp Thr Ser Ser  
 195 200 205  
 Ser Gly Glu Arg Arg Phe Gln Thr Arg Val Glu Ala Leu Arg Leu Glu  
 210 215 220  
 Arg Pro Thr Arg Gly Pro Ala Gln Ala Cys Pro Gly Arg Arg Asn Arg  
 225 230 235 240  
 Ser Arg Glu Val Gln Thr Gly Gly Val Asp Ile Asp Glu Gly Leu Glu  
 245 250 255  
 Asp Phe Pro Pro Glu Glu Asp Leu Pro Phe  
 260 265

<210> 173  
 <211> 992  
 <212> DNA  
 <213> Bacillus stearothermophilus

<400> 173

```
aattccgaca tttcaattga atcgtttatt ccgcttgaaa aagaaggcaa gttgctcggt 60
gatgtgaaaa gaccggggag catcgtactg caggcgcgct ttttctctga aatcgtgaaa 120
aaactgccgc aacaaacggt ggaaatcgaa acggaagaca actttttgac gatcatccgc 180
tcggggcact cagaattccg cctcaatggg ctaaacgccg acgaatatcc gcgcctgccg 240
caaattgaag aagaaaacgt gtttcaaadc ccggctgatt tattgaaaac cgtgattcgg 300
caaacggtgt tcgccgtttc tacatcgga acgcgcccaa tcttgacagg tgtcaactgg 360
aaagtgaac atggcgagct tgtctgcaca gcgaccgaca gtcacgcgtt agccatgcgc 420
aaagtgaaaa ttgagtcgga aaatgaagta tcatacaacg tcgtcatccc tggaaaaagt 480
cttaatgagc tcagcaaaat tttggatgac ggcaaccacc cgggtggacat cgtcatgaca 540
gccaatcaag tgctatttaa ggccgagcac cttctcttct tttcccggtt gcttgacggc 600
aactatccgg agacggcccg cttgattcca acagaaagca aaacgaccat gatcgtcaat 660
gcaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaac 720
aacgttggtg aactgacgac gcttcctgga ggaatgctcg aaatttcttc gatttctccg 780
agatcgggaa agtgacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
tttcgttcag cgcgaaatat atgatggacg cgttgccggc gcttgatgga acagacattt 900
caaatcagct tcaactgggc catgcggccg ttctgttgc gcccgcttca accgattoga 960
tgcttcagct cattttgccg gtgagaacat at 992
```

<210> 174

<211> 334

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 174

```
Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
 1             5             10             15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
      20             25             30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
      35             40             45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
      50             55             60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
      65             70             75             80

Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
      85             90             95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
      100            105            110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu
```

115	120	125
Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys		
130	135	140
Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly		
145	150	155 160
Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His		
	165	170 175
Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu		
	180	185 190
His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr		
	195	200 205
Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala		
	210	215 220
Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu		
	225	230 235 240
Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu		
	245	250 255
Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu		
	260	265 270
Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala		
	275	280 285
Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln		
	290	295 300
Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His		
	305	310 315 320
Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr		
	325	330

<210> 175  
 <211> 492  
 <212> DNA  
 <213> Bacillus stearothermophilus  
  
 <400> 175

```

atgattaacc gcgtcatttt ggtcggcagg ttaacgagag atccggagtt gcgttacact 60
ccaagcggag tggctgttgc cacgtttacg ctgcgggtca accgtccgtt tacaaatcag 120
cagggcgagc gggaaacgga ttttattcaa tgtgtcgttt ggcgccgcca ggcggaaaac 180
gtcgccaact ttttgaaaaa ggggagcttg gctggtgtcg atggccgact gcaaaccgcg 240
agctatgaaa atcaagaagg tcggcgtgtg tacgtgacgg aagtgggtggc tgatagcgtc 300
caatttcttg agccgaaagg aacgagcgag cagcgagggg cgacagcagg cggctactat 360
ggggatccat tcccattcgg gcaagatcag aaccaccaat atccgaacga aaaagggttt 420
ggccgcatcg atgacgatcc tttcgccaat gacggccagc cgatcgatat ttctgatgat 480
gatttgccgt tt 492

```

<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

```

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
  1             5             10             15

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
      20             25             30

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
      35             40             45

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
      50             55             60

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
      65             70             75             80

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
      85             90             95

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
      100            105            110

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
      115            120            125

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp
      130            135            140

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
      145            150            155            160

Asp Leu Pro Phe

```



<210> 177  
 <211> 1044  
 <212> DNA  
 <213> *Bacillus stearothermophilus*

<400> 177  
 atgctggaac gcgtatgggg aaacattgaa aaacggcggt tttctcccct ttatttatta 60  
 tacggcaatg agccgttttt attaacggaa acgtatgagc gattgggtgaa cgcagcgctt 120  
 ggccccgagg agcgggagtg gaacttggct gtgtacgact gcgaggaaac gccgatcgag 180  
 gcggcgcttg aggaggccga gacggtgccg ttttcggcg agcggcggtgt cattctcatc 240  
 aagcatccat atttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300  
 ctggaggcgt acttgaaggc gccgtcgccg ttttcgatcg tcgtcttttt cgcgcgttac 360  
 gagaagcttg atgagcgaaa aaaaattacg aagctcgcca aagagcaaag cgaagtcgtc 420  
 atcgccgccc cgctcgccga agcggagctg cgtgcctggg tgcggcgccg catcgagagc 480  
 caaggggagc aagcaagcga cgaggcgatt gatgtcctgt tgcggcgggc cgggacgcag 540  
 ctttccgcct tggcgaatga aatcgataaa ttggccctgt ttgccggatc gggcggaacc 600  
 atcgaggcgg cggcggttga gcggcttgct gcccgcacgc cggaagaaaa cgtatttgtg 660  
 cttgtcgagc aagtggcgaa gcgcgacatt ccagcagcgt tgcagacgtt ttatgatctg 720  
 cttgaaaaca atgaagagcc gatcaaaatt ttggcggttg tcgccgccca tttccgcttg 780  
 ctttcgcaag tgaaatggct tgcctcctta ggctacggac aggcgcaaatt tgctgcggcg 840  
 ctcaaggtgc acccggttccg cgtcaagctc gctcttgctc aagcggcccg cttcgctgac 900  
 ggagagcttg ctgaggcgat caacgagctc gctgacgccg attacgaagt gaaaagcggg 960  
 gcggtcgata gccggttggc cgttgagctg cttctgatgc gctggggcgc ccgcccggcg 1020  
 caagcggggc gccacggccg gcgg 1044

<210> 178  
 <211> 348  
 <212> PRT  
 <213> *Bacillus stearothermophilus*

<400> 178  
 Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro  
 1 5 10 15  
 Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr  
 20 25 30  
 Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn  
 35 40 45  
 Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu  
 50 55 60  
 Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile

65		70		75		80
Lys His Pro Tyr Phe Phe Thr Ser Glu Lys Glu Lys Glu Ile Glu His						
	85		90		95	
Asp Leu Ala Lys Leu Glu Ala Tyr Leu Lys Ala Pro Ser Pro Phe Ser						
	100		105		110	
Ile Val Val Phe Phe Ala Pro Tyr Glu Lys Leu Asp Glu Arg Lys Lys						
	115		120		125	
Ile Thr Lys Leu Ala Lys Glu Gln Ser Glu Val Val Ile Ala Ala Pro						
	130		135		140	
Leu Ala Glu Ala Glu Leu Arg Ala Trp Val Arg Arg Arg Ile Glu Ser						
145		150		155		160
Gln Gly Ala Gln Ala Ser Asp Glu Ala Ile Asp Val Leu Leu Arg Arg						
	165		170		175	
Ala Gly Thr Gln Leu Ser Ala Leu Ala Asn Glu Ile Asp Lys Leu Ala						
	180		185		190	
Leu Phe Ala Gly Ser Gly Gly Thr Ile Glu Ala Ala Ala Val Glu Arg						
	195		200		205	
Leu Val Ala Arg Thr Pro Glu Glu Asn Val Phe Val Leu Val Glu Gln						
	210		215		220	
Val Ala Lys Arg Asp Ile Pro Ala Ala Leu Gln Thr Phe Tyr Asp Leu						
225		230		235		240
Leu Glu Asn Asn Glu Glu Pro Ile Lys Ile Leu Ala Leu Leu Ala Ala						
	245		250		255	
His Phe Arg Leu Leu Ser Gln Val Lys Trp Leu Ala Ser Leu Gly Tyr						
	260		265		270	
Gly Gln Ala Gln Ile Ala Ala Ala Leu Lys Val His Pro Phe Arg Val						
	275		280		285	
Lys Leu Ala Leu Ala Gln Ala Ala Arg Phe Ala Asp Gly Glu Leu Ala						
	290		295		300	
Glu Ala Ile Asn Glu Leu Ala Asp Ala Asp Tyr Glu Val Lys Ser Gly						
305		310		315		320
Ala Val Asp Arg Arg Leu Ala Val Glu Leu Leu Leu Met Arg Trp Gly						

325

330

335

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg  
 340 345

&lt;210&gt; 179

&lt;211&gt; 757

&lt;212&gt; DNA

<213> *Bacillus stearothermophilus*

&lt;400&gt; 179

```

atgcgatggg aacagctagc gaaacgccag ccggtggtgg cgaaaatgct gcaaagcggc 60
ttggaaaaag ggcggatttc tcatgcgtac ttgtttgagg ggcagcgggg gacgggcaaa 120
aaagcggcca gtttgttggt ggcgaaacgt ttgttttgtc tgtccccaat cggagtttcc 180
ccgtgtctag agtgccgcaa ctgccggcgc atcgactccg gcaaccaccc tgacgtccgg 240
gtgatcggcc cagatggagg atcaatcaaa aaggaacaaa tcgaatggct gcagcaagag 300
ttctcgaaaa cagcggtcga gtcggataaa aaaatgtaca tcgttgagca cgccgatcaa 360
atgacgacaa gcgctgccaa cagccttctg aaatttttgg aagagccgca tccggggacg 420
gtggcggtat tgctgactga gcaataccac cgcctgctag ggacgatcgt ttcccgtgt 480
caagtgcctt cgttccggcc gttgccggcg gcagagctcg ccagggact tgtcgaggag 540
cacgtgccgt tgccgttggc gctgttggct gccatttga caaacagctt cgaggaagca 600
ctggcgcttg ccaaagatag ttggtttgcc gaggcgcgaa cattagtgt acaatggtat 660
gagatgctgg gcaagccgga gctgcagctt ttgtttttca tccacgaccg cttgtttccg 720
catttttttg aaagccatca gcttgacctt ggacttg 757

```

&lt;210&gt; 180

&lt;211&gt; 252

&lt;212&gt; PRT

<213> *Bacillus stearothermophilus*

&lt;400&gt; 180

```

Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
  1           5           10          15

Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
      20           25           30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Leu Ala
      35           40           45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
      50           55           60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
      65           70           75           80

```



```

aaaattccgg cgacgatcat ttcccgtgct caacgggttcg attttcgccg catcccgttt 540
caggcgatcg tttcacggct aaagtacgtc gcaagcgccc aaggtgtcga ggcgtcagat 600
gaggcattgt ccgccatcgc ccgtgctgca gacgggggga tgcgcgatgc gctcagcttg 660
cttgatcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720
accggggctg catcatttgc cgccttatcg agcttcatcg aagccatcca ccgcaaagat 780
acagcggcgg tttctcagca cttggaaacg atgatggcgc aagggaaaga tccgcatcgt 840
ttggttgaag acttgatttt gtactatcgc gatttattgc tgtacaaaac cgctccctat 900
gtggaggagg cgattcaaatt tgctgtcgtt gacgaagcgt tcacttcact gtcggaaatg 960
attccggttt ccaatttata cgaggccatc gagttgctga acaaaagcca gcaagagatg 1020
aagtggacaa accaccgcgc ctttctgttg gaagtggcgc ttgtgaaact ttgccatcca 1080
tcagccgccc ccccgctcgt gtccgcttcc gagttggaac cgttgataaa gcggattgaa 1140
acgctggagg cggaattgcg gcgcctgaag gaacaaccgc ctgcccctcc gtcgaccgcc 1200
gcgccggtga aaaaactgtc caaacgatg aaacggggg gatataaagc cccggttggc 1260
cgcatttacg agctgttgaa acaggcgacg catgaagatt tagctttggt gaaaggatgc 1320
tgggcgggat tgctcgacac gttgaaacgg cagcataaag tgtcgcacgc tgccttgctg 1380
caagagagcg agccggttgc agcgagcgcc tcagcgtttg tattaaaatt caaatacgaa 1440
atccactgca aaatggcgac cgatcccaca agttcgggtca aagaaaacgt cgaagcgatt 1500
ttgtttgagc tgacaaaacc cgcctttgaa atggtagcca ttccggaggg agaatgggga 1560
aaaataagag aagagttcat ccgcaataag gacgccatgg tggaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcggctgttt ggcgaagagc tgatcgaaat taaagaa 1677

```

<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

```

Val Ala Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Ala
  1              5              10              15

```

```

Asp Met Val Gly Gln Glu His Val Thr Lys Thr Leu Gln Ser Ala Leu
      20              25              30

```

```

Leu Gln His Lys Ile Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
      35              40              45

```

```

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
      50              55              60

```

```

Glu Gln Ala Pro Ala Ala Glu Pro Cys Asn Glu Cys Pro Ala Cys Leu
      65              70              75              80

```

```

Gly Ile Thr Asn Gly Thr Val Pro Asp Val Leu Glu Ile Asp Ala Ala
      85              90              95

```

```

Ser Asn Asn Arg Val Asp Glu Ile Arg Asp Ile Arg Glu Lys Val Lys
      100             105             110

```

Phe Ala Pro Thr Ser Ala Arg Tyr Lys Val Tyr Ile Ile Asp Glu Val  
115 120 125  
His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu  
130 135 140  
Glu Pro Pro Lys His Val Ile Phe Ile Leu Ala Thr Thr Glu Pro His  
145 150 155 160  
Lys Ile Pro Ala Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Arg  
165 170 175  
Arg Ile Pro Leu Gln Ala Ile Val Ser Arg Leu Lys Tyr Val Ala Ser  
180 185 190  
Ala Gln Gly Val Glu Ala Ser Asp Glu Ala Leu Ser Ala Ile Ala Arg  
195 200 205  
Ala Ala Asp Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala  
210 215 220  
Ile Ser Phe Ser Asp Gly Lys Leu Arg Leu Asp Asp Val Leu Ala Met  
225 230 235 240  
Thr Gly Ala Ala Ser Phe Ala Ala Leu Ser Ser Phe Ile Glu Ala Ile  
245 250 255  
His Arg Lys Asp Thr Ala Ala Val Leu Gln His Leu Glu Thr Met Met  
260 265 270  
Ala Gln Gly Lys Asp Pro His Arg Leu Val Glu Asp Leu Ile Leu Tyr  
275 280 285  
Tyr Arg Asp Leu Leu Leu Tyr Lys Thr Ala Pro Tyr Val Glu Gly Ala  
290 295 300  
Ile Gln Ile Ala Val Val Asp Glu Ala Phe Thr Ser Leu Ser Glu Met  
305 310 315 320  
Ile Pro Val Ser Asn Leu Tyr Glu Ala Ile Glu Leu Leu Asn Lys Ser  
325 330 335  
Gln Gln Glu Met Lys Trp Thr Asn His Pro Arg Leu Leu Leu Glu Val  
340 345 350  
Ala Leu Val Lys Leu Cys His Pro Ser Ala Ala Ala Pro Ser Leu Ser  
355 360 365

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala  
370 375 380

Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala  
385 390 395 400

Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys  
405 410 415

Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu  
420 425 430

Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu  
435 440 445

Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu  
450 455 460

Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu  
465 470 475 480

Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn  
485 490 495

Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val  
500 505 510

Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg  
515 520 525

Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala  
530 535 540

Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu  
545 550 555

<210> 183  
<211> 4301  
<212> DNA  
<213> *Bacillus stearothermophilus*

<400> 183  
atggtgacaa aagagcaaaa agagcggttt ctcacctgc ttgagcagct gaagatgacg 60  
tcggacgaat ggatgccgca ttttcgtgag gcagccattc gcaaagtcgt gatcgataaa 120  
gaggagaaaa gctggcattt ttattttcag ttcgacaacg tgctgccggt tcatgtatac 180  
aaaacgtttg ccgatcggct gcagacggcg ttccgccata tcgccgccgt ccgccatacg 240

atggagggtcg	aagcgccgcg	cgtaactgag	gcggatgtgc	aggcgtattg	gccgctttgc	300
cttgccgagc	tgcaagaagg	catgtcgccg	cttgtcgatt	ggctcagccg	gcagacgcct	360
gagctgaaaag	gaaacaagct	gcttgtcggt	gcccgccatg	aagcggaagc	gctggcgatc	420
aaacggcggt	tcgccaaaaa	aatcgctgat	gtgtacgctt	cgtttggtt	ccccccctt	480
cagcttgacg	tcagcgtcga	gccgtccaag	caagaaatgg	aacagttttt	ggcgcaaaaa	540
cagcaagagg	acgaagagcg	agcgcttgct	gtactgaccg	atttagcgag	ggaagaagaa	600
aaggccgcgt	ctgcgccgcc	gtccggtccg	cttgtcatcg	gctatccgat	ccgcgacgag	660
gagccggtgc	ggcggttga	aacgatcgtc	gaagaagagc	ggcgcgctcg	tgtgcaaggc	720
tatgtatttg	acgccgaagt	gagcgaatta	aaaagcggcc	gcacgctggt	gaccatgaaa	780
atcacagatt	acacgaactc	gatttttagtc	aaaatgttct	cgcgcgacaa	agaggacgcc	840
gagcttatga	gcggcgctcaa	aaaaggcatg	tgggtgaaaag	tgcgcggcag	cgtgcaaaac	900
gatacgttcg	tccgtgattt	ggtcatcatc	gccaacgatt	tgaacgaaat	cgccgcaaac	960
gaacggcaag	atacggcgcc	ggaaggggaa	aagagggtcg	agctccattt	gcataccccg	1020
atgagccaaa	tggacgcggt	cacctcggtg	acaaaactca	ttgagcaagc	gaaaaaatgg	1080
gggcatccgg	cgatcgccgt	caccgaccat	gccgttggtc	agtcgtttcc	ggaggcctac	1140
agcgcggcga	aaaaacacgg	catgaaggtc	atttacggcc	ttgaggcgaa	catcgtcgac	1200
gatggcggtc	cgatcgcccta	caatgagacg	caccgccgtc	tttcggagga	aacgtacgtc	1260
gtctttgacg	tcgagacgac	gggcctgtcg	gctgtgtaca	atacgatcat	tgagctggcg	1320
gcggtgaaaag	tgaaagacgg	cgagatcatc	gaccgattca	tgtcgtttgc	caaccctgga	1380
catccgttgt	cggtgacaac	gatggagctg	actgggatca	ccgatgagat	ggtgaaagac	1440
gccccgaagc	cggacgaggt	gtagcccggt	tttgttgact	gggcccgcga	tcgcacgctt	1500
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<210> 184

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

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Met Val Thr Lys Glu Gln Lys Glu Arg Phe Leu Ile Leu Leu Glu Gln
  1             5             10             15

Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
      20             25             30

Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr
      35             40             45

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
      50             55             60

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
      65             70             75             80

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
      85             90             95

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
      100            105            110

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Asp	Trp	Leu	Ser	Arg	Gln	Thr	Pro	Glu	Leu	Lys	Gly	Asn	Lys	Leu	Leu	115	120	125	
Val	Val	Ala	Arg	His	Glu	Ala	Glu	Ala	Leu	Ala	Ile	Lys	Arg	Arg	Phe	130	135	140	
Ala	Lys	Lys	Ile	Ala	Asp	Val	Tyr	Ala	Ser	Phe	Gly	Phe	Pro	Pro	Leu	145	150	155	160
Gln	Leu	Asp	Val	Ser	Val	Glu	Pro	Ser	Lys	Gln	Glu	Met	Glu	Gln	Phe	165	170	175	
Leu	Ala	Gln	Lys	Gln	Gln	Glu	Asp	Glu	Glu	Arg	Ala	Leu	Ala	Val	Leu	180	185	190	
Thr	Asp	Leu	Ala	Arg	Glu	Glu	Glu	Lys	Ala	Ala	Ser	Ala	Pro	Pro	Ser	195	200	205	
Gly	Pro	Leu	Val	Ile	Gly	Tyr	Pro	Ile	Arg	Asp	Glu	Glu	Pro	Val	Arg	210	215	220	
Arg	Leu	Glu	Thr	Ile	Val	Glu	Glu	Glu	Arg	Arg	Val	Val	Val	Gln	Gly	225	230	235	240
Tyr	Val	Phe	Asp	Ala	Glu	Val	Ser	Glu	Leu	Lys	Ser	Gly	Arg	Thr	Leu	245	250	255	
Leu	Thr	Met	Lys	Ile	Thr	Asp	Tyr	Thr	Asn	Ser	Ile	Leu	Val	Lys	Met	260	265	270	
Phe	Ser	Arg	Asp	Lys	Glu	Asp	Ala	Glu	Leu	Met	Ser	Gly	Val	Lys	Lys	275	280	285	
Gly	Met	Trp	Val	Lys	Val	Arg	Gly	Ser	Val	Gln	Asn	Asp	Thr	Phe	Val	290	295	300	
Arg	Asp	Leu	Val	Ile	Ile	Ala	Asn	Asp	Leu	Asn	Glu	Ile	Ala	Ala	Asn	305	310	315	320
Glu	Arg	Gln	Asp	Thr	Ala	Pro	Glu	Gly	Glu	Lys	Arg	Val	Glu	Leu	His	325	330	335	
Leu	His	Thr	Pro	Met	Ser	Gln	Met	Asp	Ala	Val	Thr	Ser	Val	Thr	Lys	340	345	350	
Leu	Ile	Glu	Gln	Ala	Lys	Lys	Trp	Gly	His	Pro	Ala	Ile	Ala	Val	Thr	355	360	365	

Asp His Ala Val Val Gln Ser Phe Pro Glu Ala Tyr Ser Ala Ala Lys  
 370 375 380

Lys His Gly Met Lys Val Ile Tyr Gly Leu Glu Ala Asn Ile Val Asp  
 385 390 395 400

Asp Gly Val Pro Ile Ala Tyr Asn Glu Thr His Arg Arg Leu Ser Glu  
 405 410 415

Glu Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val  
 420 425 430

Tyr Asn Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Asp Gly Glu  
 435 440 445

Ile Ile Asp Arg Phe Met Ser Phe Ala Asn Pro Gly His Pro Leu Ser  
 450 455 460

Val Thr Thr Met Glu Leu Thr Gly Ile Thr Asp Glu Met Val Lys Asp  
 465 470 475 480

Ala Pro Lys Pro Asp Glu Val Leu Ala Arg Phe Val Asp Trp Ala Gly  
 485 490 495

Asp Ala Thr Leu Val Ala His Asn Ala Ser Phe Asp Ile Gly Phe Leu  
 500 505 510

Asn Ala Gly Leu Ala Arg Met Gly Arg Gly Lys Ile Ala Asn Pro Val  
 515 520 525

Ile Asp Thr Leu Glu Leu Ala Arg Phe Leu Tyr Pro Asp Leu Lys Asn  
 530 535 540

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln  
 545 550 555 560

His His Arg Ala Ile Tyr Asp Ala Glu Ala Thr Gly His Leu Leu Met  
 565 570 575

Arg Leu Leu Lys Glu Ala Glu Glu Arg Gly Ile Leu Phe His Asp Glu  
 580 585 590

Leu Asn Ser Arg Thr His Ser Glu Ala Ser Tyr Arg Leu Ala Arg Pro  
 595 600 605

Phe His Val Thr Leu Leu Ala Gln Asn Glu Thr Gly Leu Lys Asn Leu  
 610 615 620

Phe	Lys	Leu	Val	Ser	Leu	Ser	His	Ile	Gln	Tyr	Phe	His	Arg	Val	Pro	625	630	635	640
Arg	Ile	Pro	Arg	Ser	Val	Leu	Val	Lys	His	Arg	Asp	Gly	Leu	Leu	Val	645	650	655	
Gly	Ser	Gly	Cys	Asp	Lys	Gly	Glu	Leu	Phe	Asp	Asn	Leu	Ile	Gln	Lys	660	665	670	
Ala	Pro	Glu	Glu	Val	Glu	Asp	Ile	Ala	Arg	Phe	Tyr	Asp	Phe	Leu	Glu	675	680	685	
Val	His	Pro	Pro	Asp	Val	Tyr	Lys	Pro	Leu	Ile	Glu	Met	Asp	Tyr	Val	690	695	700	
Lys	Asp	Glu	Glu	Met	Ile	Lys	Asn	Ile	Ile	Arg	Ser	Ile	Val	Ala	Leu	705	710	715	720
Gly	Glu	Lys	Leu	Asp	Ile	Pro	Val	Val	Ala	Thr	Gly	Asn	Val	His	Tyr	725	730	735	
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Gly	Gly	Ala	Asn	Pro	Leu	Asn	Arg	His	Glu	Leu	Pro	Asp	Val	Tyr	Phe	755	760	765	
Arg	Thr	Thr	Asn	Glu	Met	Leu	Asp	Cys	Phe	Ser	Phe	Leu	Gly	Pro	Glu	770	775	780	
Lys	Ala	Lys	Glu	Ile	Val	Val	Asp	Asn	Thr	Gln	Lys	Ile	Ala	Ser	Leu	785	790	795	800
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Glu	Gly	Ala	Asp	Glu	Glu	Ile	Arg	Glu	Met	Ser	Tyr	Arg	Arg	Ala	Lys	820	825	830	
Glu	Ile	Tyr	Gly	Asp	Pro	Leu	Pro	Lys	Leu	Val	Glu	Glu	Arg	Leu	Glu	835	840	845	
Lys	Glu	Leu	Lys	Ser	Ile	Ile	Gly	His	Gly	Phe	Ala	Val	Ile	Tyr	Leu	850	855	860	
Ile	Ser	His	Lys	Leu	Val	Lys	Lys	Ser	Leu	Asp	Asp	Gly	Tyr	Leu	Val	865	870	875	880

Gly Ser Arg Gly Ser Val Gly Ser Ser Phe Val Ala Thr Met Thr Glu  
                             885                            890                            895

Ile Thr Glu Val Asn Pro Leu Pro Pro His Tyr Val Cys Pro Asn Cys  
                             900                            905                            910

Lys His Ser Glu Phe Phe Asn Asp Gly Ser Val Gly Ser Gly Phe Asp  
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Leu Pro Asp Lys Asn Cys Pro Arg Cys Gly Thr Lys Tyr Lys Lys Asp  
                             930                            935                            940

Gly His Asp Ile Pro Phe Glu Thr Phe Leu Gly Phe Lys Gly Asp Lys  
 945                            950                            955                            960

Val Pro Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Pro Arg Ala  
                             965                            970                            975

His Asn Tyr Thr Lys Val Leu Phe Gly Glu Asp Asn Val Tyr Arg Ala  
                             980                            985                            990

Gly Thr Ile Gly Thr Val Ala Asp Lys Thr Ala Tyr Gly Phe Val Lys  
                             995                            1000                            1005

Ala Tyr Ala Ser Asp His Asn Leu Glu Leu Arg Gly Ala Glu Ile Asp  
                             1010                            1015                            1020

Leu Ala Ala Gly Cys Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro  
 1025                            1030                            1035                            1040

Gly Gly Ile Ile Val Val Pro Asp Tyr Met Glu Ile Tyr Asp Phe Thr  
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Pro Ile Gln Tyr Pro Ala Asp Asp Thr Ser Ser Glu Trp Arg Thr Thr  
                             1060                            1065                            1070

His Phe Asp Phe His Ser Ile His Asp Asn Leu Leu Lys Leu Asp Ile  
                             1075                            1080                            1085

Leu Gly His Asp Asp Pro Thr Val Ile Arg Met Leu Gln Asp Leu Ser  
                             1090                            1095                            1100

Gly Ile Asp Pro Lys Thr Ile Pro Thr Asp Asp Pro Asp Val Met Gly  
 1105                            1110                            1115                            1120

Ile Phe Ser Ser Thr Glu Pro Leu Gly Val Thr Pro Glu Gln Ile Met  
                             1125                            1130                            1135

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val  
 1140 1145 1150  
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 1170 1175 1180  
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 Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro  
 1205 1210 1215  
 Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Gly Leu  
 1220 1225 1230  
 Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp  
 1235 1240 1245  
 Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His  
 1250 1255 1260  
 Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val  
 1265 1270 1275 1280  
 His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu  
 1285 1290 1295  
 Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys  
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 Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu  
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 1345 1350 1355 1360  
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 1365 1370 1375  
 Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu  
 1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser  
 1395 1400 1405

Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu  
 1410 1415 1420

Pro Asp His Asn Gln Leu Ser Leu Phe  
 1425 1430

<210> 185  
 <211> 199  
 <212> PRT  
 <213> *Thermus thermophilus*

<400> 185  
 Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys  
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Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser  
 20 25 30

Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala  
 35 40 45

Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala  
 50 55 60

Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu  
 65 70 75 80

Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu  
 85 90 95

Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala  
 100 105 110

Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys  
 115 120 125

Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys  
 130 135 140

Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu  
 145 150 155 160

Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys

165

170

175

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro  
 180 185 190

Ala Gly Gln Pro Arg Val Asp  
 195

&lt;210&gt; 186

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: PCR primer

&lt;400&gt; 186

gcccagtacc tcgcctccct cgagggg

27

&lt;210&gt; 187

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: PCR primer

&lt;400&gt; 187

ggcccccttg gccttctcgg cctccat

27

&lt;210&gt; 188

&lt;211&gt; 331

&lt;212&gt; DNA

&lt;213&gt; Thermus thermophilus

&lt;400&gt; 188

agactcgagg ccctggagcg ggagctggag aagcttgccc tcctctcccc acccctcacc 60  
 ctggagaagg tggagaagggt ggtggccctg aggccccccc tcacgggctt tgacctggtg 120  
 cgctccgtcc tggagaagga cccaaggag gccctcctgc gcctcaggcg cctcaggag 180  
 gagggggagg agcccctcag gctcctcggg gccctctcct ggcagttcgc cctcctcgcc 240  
 cgggccttct tcctcctcgg ggaaaacccc aggcccaagg aggaggacct cgcccgcctc 300  
 gaggcccacc cctacgccgc caagaaggcc a 331

&lt;210&gt; 189



<211> 110  
 <212> PRT  
 <213> Thermus thermophilus

<400> 189

Arg	Leu	Glu	Ala	Leu	Glu	Arg	Glu	Leu	Glu	Lys	Leu	Ala	Leu	Leu	Ser
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Pro	Pro	Leu	Thr	Leu	Glu	Lys	Val	Glu	Lys	Val	Val	Ala	Leu	Arg	Pro
			20					25					30		
Pro	Leu	Thr	Gly	Phe	Asp	Leu	Val	Arg	Ser	Val	Leu	Glu	Lys	Asp	Pro
		35					40					45			
Lys	Glu	Ala	Leu	Leu	Arg	Leu	Arg	Arg	Leu	Arg	Glu	Glu	Gly	Glu	Glu
	50					55					60				
Pro	Leu	Arg	Leu	Leu	Gly	Ala	Leu	Ser	Trp	Gln	Phe	Ala	Leu	Leu	Ala
65					70					75					80
Arg	Ala	Phe	Phe	Leu	Leu	Arg	Glu	Asn	Pro	Arg	Pro	Lys	Glu	Glu	Asp
				85					90					95	
Leu	Ala	Arg	Leu	Glu	Ala	His	Pro	Tyr	Ala	Ala	Lys	Lys	Ala		
			100					105					110		

<210> 190  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 190

gtggtgtcta gacatcataa cggttctggc a

31

<210> 191  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 191

gagggccacc accttctcca ctttctc

27

<210> 192

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 192

ctccgtcctg gagaaggacc ccaag

25

<210> 193

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<220>

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<222> (15)

<223> S at position 15 can be either C or G

<220>

<221> primer\_bind

<222> (27)

<223> S at position 27 can be either C or G

<400> 193

cgcgaattca acgcscctct caagacsct

29

<210> 194

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 194

gacacttaac atatgggtcat cgccttcacc g

31

<210> 195  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 195  
 gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg

38

<210> 196  
 <211> 10  
 <212> PRT  
 <213> *Deinococcus radiodurans*

<400> 196  
 Val Ile Leu Asn Pro Gly Ser Val Gly Gln  
 1 5 10

<210> 197  
 <211> 10  
 <212> PRT  
 <213> *Methanococcus jannaschii*

<400> 197  
 Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln  
 1 5 10

<210> 198  
 <211> 10  
 <212> PRT  
 <213> *Thermotoga maritima*

<400> 198  
 Leu Val Leu Asn Pro Gly Ser Ala Gly Arg  
 1 5 10

<210> 199  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 199  
ctggtgaacc cgggctccgt gggccagc

28

<210> 200  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: polypeptide

<400> 200  
Leu Leu Val Asn Pro Gly Ser Val Gly Gln  
1 5 10

<210> 201  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 201  
ctcgaggagc ttgaggaggg tgttggc

27

<210> 202  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: polypeptide

<400> 202  
Ala Asn Thr Leu Leu Lys Leu Leu Glu  
1 5

<210> 203  
<211> 32  
<212> PRT

<213> *Deinococcus radiodurans*

<400> 203

Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser  
1 5 10 15

Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly  
20 25 30

<210> 204

<211> 32

<212> PRT

<213> *Caenorhabditis elegans*

<400> 204

Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser  
1 5 10 15

Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly  
20 25 30

<210> 205

<211> 32

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 205

Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser  
1 5 10 15

Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly  
20 25 30

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206

Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser  
1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly  
20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

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30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr  
1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtggggccg cgtggagctc cac

33

<210> 210  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: polypeptide

<400> 210  
Val Glu Leu His Ala Ala His Gly Tyr Leu Leu  
1 5 10

<210> 211  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 211  
ggctttccca tatggctcta caccggctc ac 32

<210> 212  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 212  
gcgtggatcc acggtcatgt ctctaagtc 29